GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 29, 2004, 10:21:11 ; Search time 547 Seconds
(without alignments)
4150.324 Million cell updates/sec

Title: US-09-830-446-27
Perfect score: 4295
Sequence: 1 MKIPLRFLLISLVPTLSMSN.....PEWRGSSRSYNVDAGSKIKF 841

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US09830446/runat_29012004_102101_19197/app_query.fasta_1.1031
-DB=N_Geneseq_19Jun03 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09830446_@CGN_1_1_0_@runat_29012004_102101_19197 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_19Jun03:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4295	100.0	2526	21	AAA28691	C. pneumoniae CPN1
2	4295	100.0	2526	24	ABL91253	Chlamydia pneumoni
3	4295	100.0	2750	21	AAA28690	C. pneumoniae CPN1
4	4278	99.6	2526	20	AAX06819	Chlamydia pneumoni
5	4255	99.1	1230025	20	AAX91990	Nucleotide sequenc
6	2603	60.6	1830	20	AAX06830	Chlamydia pneumoni
7	1580.5	36.8	3000	21	AAA27021	Chlamydia pneumoni
8	1569.5	36.5	2787	20	AAX06820	Chlamydia pneumoni
9	1497	34.9	2520	24	ABQ84758	Chlamydia psittaci
10	1497	34.9	2520	24	ABQ78016	Chlamydia polynucl
11	1497	34.9	2520	25	ABX99183	C. psittaci genomi
12	1435.5	33.4	2787	24	ABL91241	Chlamydia pneumoni
13	1435.5	33.4	2950	21	AAA30847	Chlamydia antigen
14	1435.5	33.4	3200	20	AAX06816	Chlamydia pneumoni
c 15	1435.5	33.4	273254	21	AAC81914	Chlamydia pneumoni
16	1417.5	33.0	2957	21	AAZ61509	DNA encoding the C
17	1415.5	33.0	2793	24	ABL91206	Chlamydia pneumoni
18	1409.5	32.8	3000	21	AAA30853	Chlamydia antigen
19	1407.5	32.8	2787	24	ABL91231	Chlamydia pneumoni
20	1406.5	32.7	2793	20	AAX06823	Chlamydia pneumoni
21	1406.5	32.7	2815	20	AAX06817	Chlamydia pneumoni
22	1402.5	32.7	2757	20	AAX06821	Chlamydia pneumoni
23	1390	32.4	2784	21	AAA30848	Chlamydia antigen
24	1390	32.4	273254	21	AAC81914	Chlamydia pneumoni
25	1379.5	32.1	2787	24	ABL91200	Chlamydia pneumoni
26	1377.5	32.1	2787	20	AAX06822	Chlamydia pneumoni
27	1374	32.0	2790	21	AAA30854	Chlamydia antigen
28	1372.5	32.0	2784	21	AAA30852	Chlamydia antigen
29	1372.5	32.0	2950	21	AAA30851	Chlamydia antigen
30	1370.5	31.9	2950	21	AAA30849	Chlamydia antigen
c 31	1365	31.8	1230025	20	AAX91990	Nucleotide sequenc
32	1359.5	31.7	3000	20	AAX06828	Chlamydia pneumoni
33	1357.5	31.6	2241	24	ABL91193	Chlamydia pneumoni
34	1335.5	31.1	2811	24	ABL91260	Chlamydia pneumoni
35	1335.5	31.1	3050	21	AAA48838	Chlamydia pneumoni
36	1286.5	30.0	2781	24	ABQ84775	Chlamydia psittaci
37	1286.5	30.0	2781	24	ABQ78033	Chlamydia polynucl
38	1286.5	30.0	2781	25	ABX99200	C. psittaci genomi
39	1279.5	29.8	2808	21	AAA48839	Chlamydia pneumoni
40	1274.5	29.7	2784	21	AAA30850	Chlamydia antigen
41	1198.5	27.9	3050	21	AAZ61508	DNA encoding the C
42	1170.5	27.3	2838	20	AAX06827	Chlamydia pneumoni
43	1089	25.4	2922	24	ABL91185	Chlamydia pneumoni
44	1083	25.2	3150	21	AAA27342	Chlamydia POMP91B
45	1016	23.7	2769	24	ABL91204	Chlamydia pneumoni

ALIGNMENTS

RESULT 1
AAA28691
ID AAA28691 standard; DNA; 2526 BP.
XX
AC AAA28691;
XX
DT 29-AUG-2000 (first entry)
XX
DE C. pneumoniae CPN100397 open reading frame.
XX
KW Antigen; anti-inflammatory; respiratory; antibacterial; anti-asthmatic;
KW anti-arteriosclerotic; vaccine; ds.
XX
OS Chlamydia pneumoniae.
XX
PN WO200024765-A2.
XX

PD 04-MAY-2000.
XX
PF 28-OCT-1999; 99WO-CA00992.
XX
PR 28-OCT-1998; 98US-0106034.
PR 28-OCT-1998; 98US-0106039.
PR 28-OCT-1998; 98US-0106042.
PR 28-OCT-1998; 98US-0106044.
PR 29-OCT-1998; 98US-0106072.
PR 29-OCT-1998; 98US-0106073.
PR 29-OCT-1998; 98US-0106074.
PR 29-OCT-1998; 98US-0106087.
PR 02-NOV-1998; 98US-0106587.
PR 02-NOV-1998; 98US-0106588.
PR 02-NOV-1998; 98US-0107034.
PR 02-NOV-1998; 98US-0107035.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Murdin AD, Oomen RP, Wang J;
XX
DR WPI; 2000-350688/30.
DR P-PSDB; AAY92818.
XX
PT Chlamydia antigenes and the proteins they encode, useful for
PT vaccinating against Chlamydia infections that affect the respiratory
PT tract
XX
PS Claim 2; Fig 1; 226pp; English.
XX
CC The nucleic acids may be used for the recombinant production of the
CC Chlamydia polypeptides (either in vivo or in vitro) according to standard
CC recombinant DNA methodologies. The polypeptides may then be used to
CC vaccinate against Chlamydia infections in mammals. Chlamydia, such as
CC C. pneumoniae, are pathogens responsible for upper respiratory tract
CC infections such as community acquired pneumonia, acute respiratory
CC disease and bronchitis and may be implicated in atherosclerotic changes
CC and asthma. The nucleic acids may also be used as probes for detecting
CC the presence of Chlamydia nucleic acids in samples (and therefore
CC diagnose infections) and the proteins may be used as antigens for the
CC production of antibodies that may be used to detect Chlamydia proteins
CC in samples (e.g. via enzyme linked immunosorbant assay (ELISA)).
XX
SQ Sequence 2526 BP; 693 A; 493 C; 601 G; 739 T; 0 other;

Alignment Scores:

Pred. No.:	3.12e-315	Length:	2526
Score:	4295.00	Matches:	841
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-09-830-446-27 (1-841) x AAA28691 (1-2526)

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Qy          1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
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Db          1 ATGAAGATTCCACTCCGCTTTTTATTGATATCATTAGTACCTACGCTTTCTATGTCGAAT 60

Qy         21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
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Db         61 TTATTAGGAGCTGCTACTACCGAAGAGTTATCGGCTAGCAATAGCTTCGATGGAACTACA 120

Qy         41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
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Db        121 TCAACAACAAGCTTTTCTAGTAAAACATCATCGGCTACAGATGGCACCAATTATGTTTTT 180

Qy         61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCys 80
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Db        181 AAAGATTCTGTAGTTATAGAAAATGTACCCAAAACAGGGGAAACTCAGTCTACTAGTTGT 240

Qy         81 PheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr 100
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Db        241 TTTAAAAATGACGCTGCAGCTGGAGATCTAAATTTCTTAGGAGGGGGATTTTCTTTCACA 300

Qy        101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsn 120
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Db        301 TTTAGCAATATCGATGCAACCACGGCTTCTGGAGCTGCTATTGGAAGTGAAGCAGCTAAT 360

Qy        121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
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Db        361 AAGACAGTCACGTTATCAGGATTTTCGGCACTTTCTTTTCTTAAATCCCCAGCAAGTACA 420

Qy        141 ValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAsp 160
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Db        421 GTGACTAATGGATTGGGAGCTATCAATGTTAAAGGGAATTTAAGCCTATTGGATAATGAT 480

Qy        161 LysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180
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Qy        181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArg 200
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Db        541 TCCTTGAAGATCGCAAACAATAAGTCCCTTTCTTTTATTGGAAATAGTTCTTCAACACGT 600

Qy        201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220
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Db        601 GGCGGAGCGATTCATACCAAAAACCTCACACTATCTTCTGGTGGGGAAACTCTATTTCAG 660

Qy        221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240
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Db        661 GGGAATACAGCGCCTACGGCTGCTGGTAAAGGAGGTGCTATCGCGATTGCAGACTCTGGC 720

Qy        241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260
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Db        721 ACCCTATCCATTTCTGGAGACAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCT 780

Qy        261 ThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeu 280
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Qy        281 ArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGlySerThr 300
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Db        841 CGTGCTGCGCAAGGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGACA 900

Qy        301 SerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGluTyrThr 320
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Db        901 TCTGTTGCTGATGCTCTCAATATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACG 960

Qy        321 GlyThrIleValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGluLysAsn 340
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Qy        341 ArgThrSerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLysGly 360
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Db       1021 CGCACTTCTAAATTACTTCAAAATGTTGCTTTTAAAAATGGGACTGTAGTTTTAAAAGGT 1080

Qy        361 AspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAsp 380
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Qy        381 LeuGlyThrSerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsn 400
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Qy        401 IleAspSerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAsp 420
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Qy        421 IleArgIleAspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGly 440
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Db       1261 ATTCGTATAGATCGTCCTGTTGTACTGGCAATTAGCGATGAGAGTTTTTATCAAAATGGC 1320

Qy        441 PheLeuAsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       461 ValIleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGly 480
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Qy       481 LysTrpThrIleAsnTrpSerThrAspAspLysLysAlaThrValSerTrpAlaLysGln 500
Db      1441 AAGTGGACGATCAATTGGTCTACTGATGATAAGAAAGCTACGGTTTCTTGGGCGAAGCAG 1500

Qy       501 SerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySer 520
Db      1501 AGTTTTAATCCCACTGCTGAGCAGGAGGCTCCGTTAGTTCCTAATCTTCTTTGGGGTTCT 1560

Qy       521 PheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTyr 540
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Db      1681 CAAAGGAAATTCCGTCATGTGAGTGGAGGTGCTGTAGTAGGTGCTAGCACGAGGATGCCG 1740

Qy       581 GlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPhe 600
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Qy       601 MetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSer 620
Db      1801 ATGAATACCAATTTCGCAAAGACCTACGCAGGATCTTTACGTTTGCAGCACGATGCTTCC 1860

Qy       621 LeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuPro 640
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Qy       641 TyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAsp 660
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Qy       661 HisArgMetLysThrGluSerLeuProProProProProThrLeuSerThrAspHisThr 680
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Qy       681 SerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAlaValGluAsnThr 700
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Qy       701 SerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGlnAlaValTyrAla 720
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Qy       721 ArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSerAspSerHisLeu 740
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Qy       741 TyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPheAlaGluGlnTyrTyr 760
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Qy       761 HisValValAlaMetTyrSerProAspValCysArgSerAsnProLysCysThrThrThr 780
Db      2281 CATGTTGTAGCGATGTATTCTCCAGATGTTTGTCGTAGTAACCCCAAATGTACGACTACC 2340

Qy       781 LeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAlaGly 800
Db      2341 CTACTTTCCAACCAAGGGAGTTGGAAGACCAAAGGTTCGAACTTAGCAAGACAGGCTGGT 2400

Qy       801 IleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsnPhe 820
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Qy       821 GlyPheGluTrpArgGlySerSerArgSerTyrAsnValAspAlaGlySerLysIleLys 840
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Qy       841 Phe 841
Db      2521 TTT 2523
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RESULT 2
ABL91253
ID ABL91253 standard; DNA; 2526 BP.
XX
AC ABL91253;
XX
DT 29-JUL-2002 (first entry)
XX
DE Chlamydia pneumoniae cp6270 ORF DNA, SEQ ID NO:140.
XX
KW Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KW human respiratory disease; cardiovascular disease; atherosclerosis;
KW coronary artery disease; carotid artery stenosis; myocardial infarction;
KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW strain CWL029; open reading frame; ORF; gene; ds.
XX
OS Chlamydia pneumoniae.
XX
FH Key   Location/Qualifiers
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FT   /*tag= b
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PN WO200202606-A2.
XX
PD 10-JAN-2002.
XX
PF 03-JUL-2001; 2001WO-IB01445.
XX
PR 03-JUL-2000; 2000GB-0016363.
PR 11-JUL-2000; 2000GB-0017047.
PR 21-JUL-2000; 2000GB-0017983.
PR 07-AUG-2000; 2000GB-0019368.
PR 18-AUG-2000; 2000GB-0020440.
PR 14-SEP-2000; 2000GB-0022583.
PR 10-NOV-2000; 2000GB-0027549.
PR 22-DEC-2000; 2000GB-0031706.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Ratti G, Grandi G;
XX
DR WPI; 2002-154726/20.
DR N-PSDB; ABB90595.
XX
PT Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT medicament for treatment or prevention of infection due to Chlamydia,
PT preferably Chlamydia pneumoniae, and for diagnostic purposes -
XX
PS Claim 5; Page 110-111; 364pp; English.
XX
CC Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
CC them. The proteins are predicted to be immunogenic and may therefore be
CC useful in vaccine production and for diagnostic purposes. Chlamydia
CC pneumoniae is a common cause of respiratory disease in humans, and is
CC also involved in the development of cardiovascular diseases such as
CC atherosclerosis, coronary artery disease, carotid artery stenosis,
CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
CC claudication and stroke. The proteins and nucleic acids of the invention

CC may be used in vaccines and pharmaceutical compositions for the
CC prevention or treatment of chlamydial infections, particularly Chlamydia
CC pneumoniae infections. The proteins may also be used in the detection of
CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
CC DNA probe assay or blotting techniques for determining Chlamydia
CC pneumoniae gene expression. The present sequence represents a
CC specifically claimed DNA which encodes a Chlamydia pneumoniae protein of
CC the invention.
XX
SQ Sequence 2526 BP; 693 A; 493 C; 601 G; 739 T; 0 other;

Alignment Scores:

Pred. No.:	3.12e-315	Length:	2526
Score:	4295.00	Matches:	841
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-830-446-27 (1-841) x ABL91253 (1-2526)

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Qy          1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
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Db          1 ATGAAGATTCCACTCCGCTTTTTATTGATATCATTAGTACCTACGCTTTCTATGTCGAAT 60

Qy         21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
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Db         61 TTATTAGGAGCTGCTACTACCGAAGAGTTATCGGCTAGCAATAGCTTCGATGGAACTACA 120

Qy         41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
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Db        121 TCAACAACAAGCTTTTCTAGTAAAACATCATCGGCTACAGATGGCACCAATTATGTTTTT 180

Qy         61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCys 80
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Db        181 AAAGATTCTGTAGTTATAGAAAATGTACCCAAAACAGGGGAAACTCAGTCTACTAGTTGT 240

Qy         81 PheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTAAAAATGACGCTGCAGCTGGAGATCTAAATTTCTTAGGAGGGGGATTTTCTTTCACA 300

Qy        101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsn 120
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Qy        121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
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Db        361 AAGACAGTCACGTTATCAGGATTTTCGGCACTTTCTTTTCTTAAATCCCCAGCAAGTACA 420

Qy        141 ValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAsp 160
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Qy        161 LysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180
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Db        481 AAGGTATTGATTCAGGACAATTTCTCAACAGGAGATGGCGGAGCAATTAATTGTGCAGGC 540

Qy        181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArg 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTTGAAGATCGCAAACAATAAGTCCCTTTCTTTTATTGGAAATAGTTCTTCAACACGT 600

Qy        201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220
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Qy        221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240
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Qy        241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260
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Qy        261 ThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeu 280
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Db        781 ACAGGAACCGTCTCTCATAGTGCTATTGATTTAGGAACTAGCGCTAAGATAACTGCGTTA 840

Qy        281 ArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGlySerThr 300
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Db        841 CGTGCTGCGCAAGGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGACA 900

Qy        301 SerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGluTyrThr 320
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Qy        321 GlyThrIleValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGluLysAsn 340
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Qy        341 ArgThrSerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLysGly 360
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Qy        361 AspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAsp 380
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Qy        381 LeuGlyThrSerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsn 400
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Db       1141 TTAGGGACGTCGTTGGTTGCAAACACCGAAAGTATCGAGTTAACGAATTTGGAAATTAAT 1200

Qy        401 IleAspSerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAsp 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 ATAGACTCTCTCAGGAACGGGAAAAAGATAAAACTCAGTGCTGCCACAGCTCAGAAAGAT 1260

Qy        421 IleArgIleAspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGly 440
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Qy        441 PheLeuAsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIle 460
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Qy        461 ValIleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGly 480
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Db       1381 GTGATTTCTGCAGATTCTCGCAGTATAGATGCTGTACAATCTCCGTATGGCTATCAGGGA 1440

Qy        481 LysTrpThrIleAsnTrpSerThrAspAspLysLysAlaThrValSerTrpAlaLysGln 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAGTGGACGATCAATTGGTCTACTGATGATAAGAAAGCTACGGTTTCTTGGGCGAAGCAG 1500

Qy        501 SerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySer 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AGTTTTAATCCCACTGCTGAGCAGGAGGCTCCGTTAGTTCCTAATCTTCTTTGGGGTTCT 1560

Qy        521 PheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTyr 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        541 GluLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAsn 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GAAAAGAGATTTTGGGTTGCAGGCATTTCCAATGTTTTGCATAGGAGCGGTCGTGAAAAT 1680

Qy        561 GlnArgLysPheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArgMetPro 580
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Qy        601 MetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSer 620
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Qy        621 LeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuPro 640
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Qy        641 TyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAsp 660
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Qy        701 SerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGlnAlaValTyrAla 720
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Db       2101 AGCGGCAGAGGATTTTTCCAAGAGTACACTCCATTTGTAAAAGTCCAAGCTGTTTACGCT 2160

Qy        721 ArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSerAspSerHisLeu 740
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Qy        741 TyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPheAlaGluGlnTyrTyr 760
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Qy        781 LeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAlaGly 800
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Qy        801 IleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsnPhe 820
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Qy        821 GlyPheGluTrpArgGlySerSerArgSerTyrAsnValAspAlaGlySerLysIleLys 840
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Db       2461 GGCTTTGAATGGCGGGGATCTTCTCGTAGCTATAATGTAGATGCGGGTAGCAAAATCAAA 2520

Qy        841 Phe 841
                    |||
Db       2521 TTT 2523
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RESULT 3
AAA28690
ID AAA28690 standard; DNA; 2750 BP.
XX
AC AAA28690;
XX
DT 29-AUG-2000 (first entry)
XX
DE C. pneumoniae CPN100397 gene.
XX
KW Antigen; anti-inflammatory; respiratory; antibacterial; anti-asthmatic;
KW anti-arteriosclerotic; vaccine; ds.
XX
OS Chlamydia pneumoniae.
XX
FH Key   Location/Qualifiers
FT CDS   101..2626
FT   /*tag= a
XX
PN WO200024765-A2.
XX
PD 04-MAY-2000.
XX
PF 28-OCT-1999; 99WO-CA00992.
XX
PR 28-OCT-1998; 98US-0106034.
PR 28-OCT-1998; 98US-0106039.
PR 28-OCT-1998; 98US-0106042.
PR 28-OCT-1998; 98US-0106044.
PR 29-OCT-1998; 98US-0106072.
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PR 29-OCT-1998; 98US-0106074.
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PR 02-NOV-1998; 98US-0106587.
PR 02-NOV-1998; 98US-0106588.
PR 02-NOV-1998; 98US-0107034.
PR 02-NOV-1998; 98US-0107035.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Murdin AD, Oomen RP, Wang J;
XX
DR WPI; 2000-350688/30.
DR P-PSDB; AAY92818.
XX
PT Chlamydia antigenes and the proteins they encode, useful for
PT vaccinating against Chlamydia infections that affect the respiratory
PT tract
XX
PS Claim 2; Fig 1; 226pp; English.
XX
CC The nucleic acids may be used for the recombinant production of the
CC Chlamydia polypeptides (either in vivo or in vitro) according to standard
CC recombinant DNA methodologies. The polypeptides may then be used to
CC vaccinate against Chlamydia infections in mammals. Chlamydia, such as
CC C. pneumoniae, are pathogens responsible for upper respiratory tract
CC infections such as community acquired pneumonia, acute respiratory
CC disease and bronchitis and may be implicated in atherosclerotic changes
CC and asthma. The nucleic acids may also be used as probes for detecting
CC the presence of Chlamydia nucleic acids in samples (and therefore
CC diagnose infections) and the proteins may be used as antigens for the
CC production of antibodies that may be used to detect Chlamydia proteins
CC in samples (e.g. via enzyme linked immunosorbant assay (ELISA)).
XX
SQ Sequence 2750 BP; 756 A; 532 C; 641 G; 821 T; 0 other;

Alignment Scores:

Pred. No.:	3.47e-315	Length:	2750
Score:	4295.00	Matches:	841
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-09-830-446-27 (1-841) x AAA28690 (1-2750)

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Qy          1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
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Qy         21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
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Qy         61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCys 80
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Qy        101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsn 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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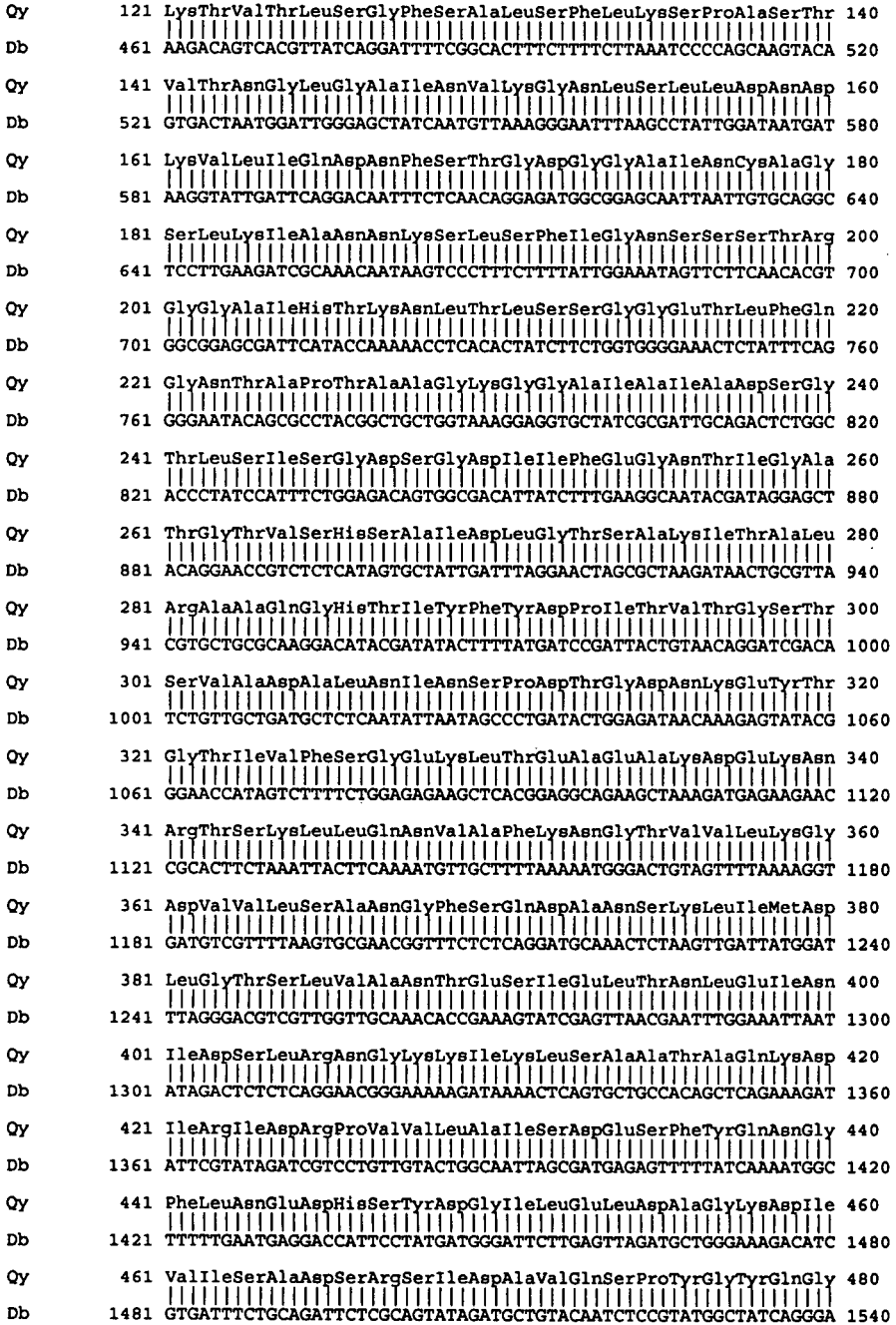
Qy 121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
Db 461 AAGACAGTCACGTTATCAGGATTTTCGGCACTTTCTTTTCTTAAATCCCCAGCAAGTACA 520
Qy 141 ValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAsp 160
Db 521 GTGACTAATGGATTGGGAGCTATCAATGTTAAAGGGAATTTAAGCCTATTGGATAATGAT 580
Qy 161 LysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180
Db 581 AAGGTATTGATTCAGGACAATTTCTCAACAGGAGATGGCGGAGCAATTAATTGTGCAGGC 640
Qy 181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArg 200
Db 641 TCCTTGAAGATCGCAAACAATAAGTCCCTTTCTTTTATTGGAAATAGTTCTTCAACACGT 700
Qy 201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220
Db 701 GGCGGAGCGATTCATACCAAAAACCTCACACTATCTTCTGGTGGGGAAACTCTATTTCAG 760
Qy 221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240
Db 761 GGGAATACAGCGCCTACGGCTGCTGGTAAAGGAGGTGCTATCGCGATTGCAGACTCTGGC 820
Qy 241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260
Db 821 ACCCTATCCATTTCTGGAGACAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCT 880
Qy 261 ThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeu 280
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Qy 281 ArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGlySerThr 300
Db 941 CGTGCTGCGCAAGGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGACA 1000
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Db 1001 TCTGTTGCTGATGCTCTCAATATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACG 1060
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Db 1241 TTAGGGACGTCGTTGGTTGCAAACACCGAAAGTATCGAGTTAACGAATTTGGAAATTAAT 1300
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Qy 421 IleArgIleAspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGly 440
Db 1361 ATTCGTATAGATCGTCCTGTTGTACTGGCAATTAGCGATGAGAGTTTTTATCAAAATGGC 1420
Qy 441 PheLeuAsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIle 460
Db 1421 TTTTTGAATGAGGACCATTCCTATGATGGGATTCTTGAGTTAGATGCTGGGAAAGACATC 1480
Qy 461 ValIleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGly 480
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Qy 521 PheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTyr 540
Db 1661 TTTATAGATGTTCGTTCCTTCCAGAATTTTATAGAGCTAGGTACTGAAGGTGCTCCTTAC 1720
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Db 1721 GAAAAGAGATTTTGGGTTGCAGGCATTTCCAATGTTTTGCATAGGAGCGGTCGTGAAAAT 1780
Qy 561 GlnArgLysPheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArgMetPro 580
Db 1781 CAAAGGAAATTCCGTCATGTGAGTGGAGGTGCTGTAGTAGGTGCTAGCACGAGGATGCCG 1840
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Db 1841 GGTGGTGATACCTTGTCTCTGGGTTTTGCTCAGCTCTTTGCGCGTGACAAAGACTACTTT 1900
Qy 601 MetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSer 620
Db 1901 ATGAATACCAATTTCGCAAAGACCTACGCAGGATCTTTACGTTTGCAGCACGATGCTTCC 1960
Qy 621 LeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuPro 640
Db 1961 CTATACTCTGTGGTGAGTATCCTTTTAGGAGAGGGAGGACTCCGCGAGATCCTGTTGCCT 2020
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Qy 681 SerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAlaValGluAsnThr 700
Db 2141 TCTTGGGGAGGATATGTCTGGGCTGGAGAGCTGGGAACTCGAGTTGCTGTTGAAAATACC 2200
Qy 701 SerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGlnAlaValTyrAla 720
Db 2201 AGCGGCAGAGGATTTTTCCAAGAGTACACTCCATTTGTAAAAGTCCAAGCTGTTTACGCT 2260
Qy 721 ArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSerAspSerHisLeu 740
Db 2261 CGCCAAGATAGCTTTGTAGAACTAGGAGCTATCAGTCGTGATTTTAGTGATTCGCATCTT 2320
Qy 741 TyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPheAlaGluGlnTyrTyr 760
Db 2321 TATAACCTTGCGATTCCTCTTGGAATCAAGTTAGAGAAACGGTTTGCAGAGCAATATTAT 2380
Qy 761 HisValValAlaMetTyrSerProAspValCysArgSerAsnProLysCysThrThrThr 780
Db 2381 CATGTTGTAGCGATGTATTCTCCAGATGTTTGTCGTAGTAACCCCAAATGTACGACTACC 2440
Qy 781 LeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAlaGly 800
Db 2441 CTACTTTCCAACCAAGGGAGTTGGAAGACCAAAGGTTCGAACTTAGCAAGACAGGCTGGT 2500
Qy 801 IleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsnPhe 820
Db 2501 ATTGTTCAGGCCTCAGGTTTTCGATCTTTGGGAGCTGCAGCAGAGCTTTTCGGGAACTTT 2560
Qy 821 GlyPheGluTrpArgGlySerSerArgSerTyrAsnValAspAlaGlySerLysIleLys 840
Db 2561 GGCTTTGAATGGCGGGGATCTTCTCGTAGCTATAATGTAGATGCGGGTAGCAAAATCAAA 2620
Qy 841 Phe 841

```
Db       2621 TTT 2623

RESULT 4
AAX06819
ID   AAX06819 standard; DNA; 2526 BP.
XX
AC   AAX06819;
XX
DT   26-APR-1999  (first entry)
XX
DE   Chlamydia pneumoniae surface exposed protein Omp7 DNA.
XX
KW   Omp7; outer membrane protein 7; surface exposed protein; antigen;
KW   infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
XX
OS   Chlamydia pneumoniae.
XX
PN   WO9858953-A2.
XX
PD   30-DEC-1998.
XX
PF   19-JUN-1998;   98WO-DK00266.
XX
PR   23-JUN-1997;   97DK-0000744.
XX
PA   (BIRK/) BIRKELUND S.
PA   (CHRI/) CHRISTIANSEN G.
XX
PI   Birkelund S,  Christiansen G,  Knudsen K,  Madsen A;
PI   Mygind P;
XX
DR   WPI; 1999-105610/09.
DR   P-PSDB; AAW88420.
XX
PT   Species-specific test for identifying mammals infected with
PT   Chlamydia pneumoniae - comprises detecting antibodies specific for
PT   outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT   these proteins
XX
PS   Claim 6; Page 49-50; 115pp; English.
XX
CC   This DNA sequence codes for the novel 89.7 kDa surface exposed
CC   protein Omp7 (see AAW88420) of the human respiratory pathogen
CC   Chlamydia pneumoniae.  By generating antibodies against C.
CC   pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
CC   was obtained which reacted with outer membrane proteins.  The
CC   antibody was used to identify the genes (see AAX06816-27) encoding
CC   Omp4-Omp15 proteins (see AAW88417-28) in an expression library of
CC   C. pneumoniae DNA.  The genes are situated in 2 gene clusters:
CC   Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
CC   the other, and encode polypeptides of about 89.6-100.3 kDa and
CC   about 56.1 kDa.  The invention provides a new species specific test
CC   for identifying mammals (including humans) infected with Chlamydia
CC   pneumoniae.  The test comprises detecting antibodies specific for
CC   Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC   membrane proteins, especially by PCR.  The proteins are also used
CC   in the diagnosis of C. pneumoniae infection in mammals.  The
CC   nucleic acids and proteins can also be used in the immunization of
CC   mammals, the nucleic acids being particularly useful as DNA
CC   vaccines for effecting in vivo expression of antigens.  The
CC   vaccines may also prevent atherosclerosis and bronchial asthma,
CC   which are possibly associated with C. pneumoniae.
XX
SQ   Sequence 2526 BP; 696 A; 495 C; 597 G; 738 T; 0 other;

Alignment Scores:
Pred. No.:              6.04e-314       Length:         2526
Score:                  4278.00         Matches:        837
Percent Similarity:     99.88%          Conservative:   3
Best Local Similarity:  99.52%          Mismatches:     1
Query Match:            99.60%          Indels:         0
DB:                     20              Gaps:           0

US-09-830-446-27 (1-841) x AAX06819 (1-2526)

Qy          1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAGATTCCACTCCGCTTTTTATTGATATCATTAGTACCTACGCTTTCTATGTCGAAT 60

Qy         21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTATTAGGAGCTGCTACTACCGAAGAGCTATCGGCTAGCAATAGCTTCGATGGAACTACA 120

Qy         41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCAACAACAAGCTTTTCTAGTAAAACATCATCGGCTACAGATGGCACCAATTATGTTTTT 180

Qy         61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGATTCTGTAGTTATAGAAAATGTACCCAAAACAGGGGAAACTCAGTCTACTAGTTGT 240

Qy         81 PheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTAAAAATGACGCTGCAGCTGGAGATCTAAATTTCTTAGGAGGGGGATTTTCTTTCACA 300

Qy        101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTAGCAATATCGATGCAACCACGGCTTCTGGAGCTGCTATTGGAAGTGAAGCAGCTAAT 360

Qy        121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAGACAGTCACGTTATCAGGATTTTCGGCACTTTCTTTTCTTAAATCCCCAGCAAGTACA 420

Qy        141 ValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAsp 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGACTAATGGATTGGGAGCTATCAATGTTAAAGGGAATTTAAGCCTATTGGATAATGAT 480

Qy        161 LysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAGGTATTGATTCAGGACAATTTCTCAACAGGAGATGGCGGAGCAATTAATTGTGCAGGC 540

Qy        181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArg 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTTGAAGATCGCAAACAATAAGTCCCTTTCTTTTATTGGAAATAGTTCTTCAACACGT 600

Qy        201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGCGGAGCGATTCATACCAAAAACCTCACACTATCTTCTGGTGGGGAAACTCTATTTCAG 660

Qy        221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAATACAGCGCCTACGGCTGCTGGTAAAGGAGGTGCTATCGCGATTGCAGACTCTGGC 720

Qy        241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCCTATCCATTTCTGGAGACAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCT 780

Qy        261 ThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACAGGAACCGTCTCTCATAGTGCTATTGATTTAGGAACTAGCGCTAAGATAACTGCGTTA 840

Qy        281 ArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGlySerThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGTGCTGCGCAAGGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGACA 900

Qy        301 SerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGluTyrThr 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCTGTTGCTGATGCTCTCAATATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACG 960

Qy        321 GlyThrIleValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGluLysAsn 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGAACCATAGTCTTTTCTGGAGAGAAGCTCACGGAGGCAGAAGCTAAAGATGAGAAGAAC 1020

Qy        341 ArgThrSerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLysGly 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1021 CGCACTTCTAAATTACTTCAAAATGTTGCTTTTAAAAATGGGACTGTAGTTTTAAAAGGT 1080

Qy        361 AspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAsp 380

Db       1081 GATGTCGTTTTAAGTGCGAACGGTTTCTCTCAGGATGCAAACTCTAAGTTGATTATGGAT 1140

Qy        381 LeuGlyThrSerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsn 400

Db       1141 TTAGGGACGTCGTTGGTTGCAAACACCGAAAGTATCGAGTTAACGAATTTGGAAATTAAT 1200

Qy        401 IleAspSerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAsp 420

Db       1201 ATAGACTCTCTCAGGAACGGGAAAAAGATAAAACTCAGTGCTGCCACAGCTCAGAAAGAT 1260

Qy        421 IleArgIleAspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGly 440

Db       1261 ATTCGTATAGATCGTCCTGTTGTACTGGCAATTAGCGATGAGAGTTTTTATCAAAATGGC 1320

Qy        441 PheLeuAsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIle 460

Db       1321 TTTTTGAATGAGGACCATTCCTATGATGGGATTCTTGAGTTAGATGCTGGGAAAGACATC 1380

Qy        461 ValIleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGly 480

Db       1381 GTGATTTCTGCAGATTCTCGCAGTATAAATGCTGTACAATCTCCGTATGGCTATCAGGGA 1440

Qy        481 LysTrpThrIleAsnTrpSerThrAspAspLysLysAlaThrValSerTrpAlaLysGln 500

Db       1441 AAGTGGACAATCAATTGGTCTACTGATGATAAGAAAGCTACGGTTTCTTGGGCAAAGCAA 1500

Qy        501 SerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySer 520

Db       1501 AGTTTTAATCCCACTGCTGAGCAGGAGGCTCCGTTAGTTCCTAATCTTCTTTGGGGTTCT 1560

Qy        521 PheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTyr 540

Db       1561 TTTATAGATGTTCGTCCCTTCCAAAATTTTATAGAGCTAGGTACTGAAGGTGCTCCTTAC 1620

Qy        541 GluLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAsn 560

Db       1621 GAAAAGAGATTTTGGGTTGCAGGCATTTCCAATGTTTTGCATAGGAGCGGTCGTGAAAAT 1680

Qy        561 GlnArgLysPheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArgMetPro 580

Db       1681 CAAAGGAAATTCCGTCATGTGAGTGGAGGTGCTGTAGTAGGTGCTAGCACGAGGATGCCG 1740

Qy        581 GlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPhe 600

Db       1741 GGTGGTGATACCTTGTCTCTGGGTTTTGCTCAGCTCTTTGCGCGTGACAAAGACTACTTT 1800

Qy        601 MetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSer 620

Db       1801 ATGAATACCAATTTCGCAAAGACCTACGCAGGATCTTTACGTTTGCAGCACGATGCTTCC 1860

Qy        621 LeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuPro 640

Db       1861 CTATACTCTGTGGTGAGTATCCTTTTAGGAGAGGGAGGACTCCGCGAGATCCTGTTGCCT 1920

Qy        641 TyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAsp 660

Db       1921 TATGTTTCCAAGACTCTGCCGTGCTCTTTCTATGGGCAGCTTAGCTACGGCCATACGGAT 1980

Qy        661 HisArgMetLysThrGluSerLeuProProProProProThrLeuSerThrAspHisThr 680

Db       1981 CATCGCATGAAGACCGAGTCTCTACCCCCCCCCCCCCCGACGCTCTCGACGGATCATACT 2040

Qy        681 SerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAlaValGluAsnThr 700

Db       2041 TCTTGGGGAGGATATGTCTGGGCTGGAGAGCTGGGAACTCGAGTTGCTGTTGAAAATACC 2100

Qy        701 SerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGlnAlaValTyrAla 720

Db       2101 AGCGGCAGAGGATTTTTCCGAGAGTACACTCCATTTGTAAAAGTCCAAGCTGTTTACTCG 2160

Qy        721 ArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSerAspSerHisLeu 740

Db       2161 CGCCAAGATAGCTTTGTTGAACTAGGAGCTATCAGTCGTGATTTTAGTGATTCGCATCTT 2220

Qy        741 TyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPheAlaGluGlnTyrTyr 760

Db       2221 TATAACCTTGCGATTCCTCTTGGAATCAAGTTAGAGAAACGGTTTGCAGAGCAATATTAT 2280

Qy        761 HisValValAlaMetTyrSerProAspValCysArgSerAsnProLysCysThrThrThr 780

Db       2281 CATGTTGTAGCGATGTATTCTCCAGATGTTTGTCGTAGTAACCCCAAATGTACGACTACC 2340

Qy        781 LeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAlaGly 800

Db       2341 CTACTTTCCAACCAAGGGAGTTGGAAGACCAAAGGTTCGAACTTAGCAAGACAGGCTGGT 2400

Qy        801 IleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsnPhe 820

Db       2401 ATTGTTCAGGCCTCAGGTTTTCGATCTTTGGGAGCTGCAGCAGAGCTTTTCGGGAACTTT 2460

Qy        821 GlyPheGluTrpArgGlySerSerArgSerTyrAsnValAspAlaGlySerLysIleLys 840

Db       2461 GGCTTTGAATGGCGGGGATCTTCTCGTAGCTATAATGTAGATGCGGGTAGCAAAATCAAA 2520

Qy        841 Phe 841

Db       2521 TTT 2523
```

RESULT 5
AAX91990
ID AAX91990 standard; DNA; 1230025 BP.
XX
AC AAX91990;
XX
DT 13-SEP-1999 (first entry)
XX
DE Nucleotide sequence of the complete genome of Chlamydia pneumoniae.
XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope; ss.
XX
OS Chlamydia pneumoniae.
XX
PN WO9927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98WO-IB01890.
XX
PR 04-NOV-1998; 98US-0107078.
PR 21-NOV-1997; 97FR-0014673.
XX
PA (GEST) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-357842/30.
XX
PT Genome sequence of Chlamydia pneumoniae
XX
PS Claim 1; Page 291-611; 1912pp; English.
XX
CC The present sequence represents the complete genome of Chlamydia
CC pneumoniae, and encodes proteins AAY34584-Y35879. C. pneumoniae causes
CC respiratory disease such as pneumonia and bronchitis and is thought
CC to be a contributing factor in heart disease, sarcoidosis, sinusitis,
CC purulent otitis media, erythema nodosum or pharyngitis. The polypeptides
CC encoded by the open reading frames of the C. pneumoniae genome (see
CC AAY34584-Y35879) can be used in immunogenic compositions as vaccines.
CC Vectors containing C. pneumoniae nucleotides sequences can also be
CC used as immunogenic compositions, especially where the vector directs

```
CC   the expression of a neutralising epitope of C. pneumoniae.
XX
SQ   Sequence 1230025 BP; 367213 A; 249833 C; 249013 G; 363589 T; 377 other;

Alignment Scores:
Pred. No.:                8e-309        Length:          1230025
Score:                    4255.00       Matches:         840
Percent Similarity:       99.76%        Conservative:    0
Best Local Similarity:    99.76%        Mismatches:      1
Query Match:              99.07%        Indels:          2
DB:                       20            Gaps:            0

US-09-830-446-27 (1-841) x AAX91990 (1-1230025)

Qy          1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28950 ATGAAGATTCCACTCCGCTTTTTATTGATATCATTAGTACCTACGCTTTCTATGTCGAAT 29009

Qy         21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29010 TTATTAGGAGCTGCTACTACCGAAGAGTTATCGGCTAGCAATAGCTTCGATGGAACTACA 29069

Qy         41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29070 TCAACAACAAGCTTTTCTAGTAAAACATCATCGGCTACAGATGGCACCAATTATGTTTTT 29129

Qy         61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29130 AAAGATTCTGTAGTTATAGAAAATGTACCCAAAACAGGGGAAACTCAGTCTACTAGTTGT 29189

Qy         81 PheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29190 TTTAAAAATGACGCTGCAGCTGGAGATCTAAATTTCTTAGGAGGGGGATTTTCTTTCACA 29249

Qy        101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29250 TTTAGCAATATCGATGCAACCACGGCTTCTGGAGCTGCTATTGGAAGTGAAGCAGCTAAT 29309

Qy        121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29310 AAGACAGTCACGTTATCAGGATTTTCGGCACTTTCTTTTCTTAAATCCCCAGCAAGTACA 29369

Qy        141 ValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAsp 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29370 GTGACTAATGGATTGGGAGCTATCAATGTTAAAGGGAATTTAAGCCTATTGGATAATGAT 29429

Qy        161 LysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db      29430 AAGGTATTGATTCAGGACAATTTCTCAACAGGAGATGGCGGACA-ATTAATTGTGCAGGC 29488

Qy        181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArg 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29489 TCCTTGAAGATCGCAAACAATAAGTCCCTTTCTTTTATTGGAAATAGTTCTTCAACACGT 29548

Qy        201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29549 GGCGGAGCGATTCATACCAAAAACCTCACACTATCTTCTGGTGGGGAAACTCTATTTCAG 29608

Qy        221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29609 GGGAATACAGCGCCTACGGCTGCTGGTAAAGGAGGTGCTATCGCGATTGCAGACTCTGGC 29668

Qy        241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29669 ACCCTATCCATTTCTGGAGACAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCT 29728

Qy        261 ThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29729 ACAGGAACCGTCTCTCATAGTGCTATTGATTTAGGAACTAGCGCTAAGATAACTGCGTTA 29788

Qy        281 ArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGlySerThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29789 CGTGCTGCGCAAGGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGACA 29848

Qy        301 SerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGluTyrThr 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29849 TCTGTTGCTGATGCTCTCAATATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACG 29908

Qy        321 GlyThrIleValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGluLysAsn 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29909 GGAACCATAGTCTTTTCTGGAGAGAAGCTCACGGAGGCAGAAGCTAAAGATGAGAAGAAC 29968

Qy        341 ArgThrSerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeu-LysGl 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db      29969 CGCACTTCTAAATTACTTCAAAATGTTGCTTTTAAAAATGGGACTGTAGTTTTGAAAAGG 30028

Qy        360 yAspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAs 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30029 TGATGTCGTTTTAAGTGCGAACGGTTTCTCTCAGGATGCAAACTCTAAGTTGATTATGGA 30088

Qy        380 pLeuGlyThrSerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAs 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30089 TTTAGGGACGTCGTTGGTTGCAAACACCGAAAGTATCGAGTTAACGAATTTGGAAATTAA 30148

Qy        400 nIleAspSerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAs 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30149 TATAGACTCTCTCAGGAACGGGAAAAAGATAAAACTCAGTGCTGCCACAGCTCAGAAAGA 30208

Qy        420 pIleArgIleAspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGl 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30209 TATTCGTATAGATCGTCCTGTTGTACTGGCAATTAGCGATGAGAGTTTTTATCAAAATGG 30268

Qy        440 yPheLeuAsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIl 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30269 CTTTTTGAATGAGGACCATTCCTATGATGGGATTCTTGAGTTAGATGCTGGGAAAGACAT 30328

Qy        460 eValIleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGl 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30329 CGTGATTTCTGCAGATTCTCGCAGTATAGATGCTGTACAATCTCCGTATGGCTATCAGGG 30388

Qy        480 yLysTrpThrIleAsnTrpSerThrAspAspLysLysAlaThrValSerTrpAlaLysGl 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30389 AAAGTGGACGATCAATTGGTCTACTGATGATAAGAAAGCTACGGTTTCTTGGGCGAAGCA 30448

Qy        500 nSerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySe 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30449 GAGTTTTAATCCCACTGCTGAGCAGGAGGCTCCGTTAGTTCCTAATCTTCTTTGGGGTTC 30508

Qy        520 rPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTy 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30509 TTTTATAGATGTTCGTTCCTTCCAGAATTTTATAGAGCTAGGTACTGAAGGTGCTCCTTA 30568

Qy        540 rGluLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAs 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30569 CGAAAAGAGATTTTGGGTTGCAGGCATTTCCAATGTTTTGCATAGGAGCGGTCGTGAAAA 30628

Qy        560 nGlnArgLysPheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArgMetPr 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30629 TCAAAGGAAATTCCGTCATGTGAGTGGAGGTGCTGTAGTAGGTGCTAGCACGAGGATGCC 30688

Qy        580 oGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPh 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30689 GGGTGGTGATACCTTGTCTCTGGGTTTTGCTCAGCTCTTTGCGCGTGACAAAGACTACTT 30748

Qy        600 eMetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30749 TATGAATACCAATTTCGCAAAGACCTACGCAGGATCTTTACGTTTGCAGCACGATGCTTC 30808

Qy        620 rLeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuPr 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30809 CCTATACTCTGTGGTGAGTATCCTTTTAGGAGAGGGAGGACTCCGCGAGATCCTGTTGCC 30868

Qy        640 oTyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAs 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30869 TTATGTTTCCAAGACTCTGCCGTGCTCTTTCTATGGGCAGCTTAGCTACGGCCATACGGA 30928
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Qy        660 pHisArgMetLysThrGluSerLeuProProProProProThrLeuSerThrAspHisTh 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30929 TCATCGCATGAAGACCGAGTCTCTACCCCCCCCCCCCCCCGACGCTCTCGACGGATCATAC 30988

Qy        680 rSerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAlaValGluAsnTh 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30989 TTCTTGGGGAGGATATGTCTGGGCTGGAGAGCTGGGAACTCGAGTTGCTGTTGAAAATAC 31048

Qy        700 rSerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGlnAlaValTyrAl 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      31049 CAGCGGCAGAGGATTTTTCCAAGAGTACACTCCATTTGTAAAAGTCCAAGCTGTTTACGC 31108

Qy        720 aArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSerAspSerHisLe 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      31109 TCGCCAAGATAGCTTTGTAGAACTAGGAGCTATCAGTCGTGATTTTAGTGATTCGCATCT 31168

Qy        740 uTyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPheAlaGluGlnTyrTy 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      31169 TTATAACCTTGCGATTCCTCTTGGAATCAAGTTAGAGAAACGGTTTGCAGAGCAATATTA 31228

Qy        760 rHisValValAlaMetTyrSerProAspValCysArgSerAsnProLysCysThrThrTh 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      31229 TCATGTTGTAGCGATGTATTCTCCAGATGTTTGTCGTAGTAACCCCAAATGTACGACTAC 31288

Qy        780 rLeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAlaGl 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      31289 CCTACTTTCCAACCAAGGGAGTTGGAAGACCAAAGGTTCGAACTTAGCAAGACAGGCTGG 31348

Qy        800 yIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsnPh 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      31349 TATTGTTCAGGCCTCAGGTTTTCGATCTTTGGGAGCTGCAGCAGAGCTTTTCGGGAACTT 31408

Qy        820 eGlyPheGluTrpArgGlySerSerArgSerTyrAsnValAspAlaGlySerLysIleLy 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      31409 TGGCTTTGAATGGCGGGGATCTTCTCGTAGCTATAATGTAGATGCGGGTAGCAAAATCAA 31468

Qy        840 sPhe 841
              ||||
Db      31469 ATTT 31472
```

RESULT 6
AAX06830

ID AAX06830 standard; DNA; 1830 BP.
XX
AC AAX06830;
XX
DT 26-APR-1999 (first entry)
XX
DE Chlamydia pneumoniae surface exposed protein Omp7 DNA.
XX
KW Omp7; outer membrane protein 7; surface exposed protein; antigen;
KW infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
XX
OS Chlamydia pneumoniae.
XX
PN WO9858953-A2.
XX
PD 30-DEC-1998.
XX
PF 19-JUN-1998; 98WO-DK00266.
XX
PR 23-JUN-1997; 97DK-0000744.
XX
PA (BIRK/) BIRKELUND S.
PA (CHRI/) CHRISTIANSEN G.
XX
PI Birkelund S, Christiansen G, Knudsen K, Madsen A;
PI Mygind P;
XX
DR WPI; 1999-105610/09.
DR P-PSDB; AAW88431.
XX
PT Species-specific test for identifying mammals infected with
PT Chlamydia pneumoniae - comprises detecting antibodies specific for
PT outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT these proteins
XX
PS Disclosure; Page 83-86; 115pp; English.
XX
CC This DNA sequence encodes the novel surface exposed protein Omp7
CC (see AAW88431) of Chlamydia pneumoniae, a human respiratory pathogen.
CC It is described as a subsequence of a claimed nucleic acid fragment
CC (see AAX06819) encoding Omp7 (see AAW88420). The invention provides a
CC new species specific test for identifying mammals (including
CC humans) infected with C. pneumoniae. The test comprises detecting
CC antibodies specific for surface exposed proteins Omp4-Omp15 (see
CC AAW88417-28) or detecting nucleic acid fragments encoding them (see
CC AAX06816-27), especially by PCR. The proteins are also used in the
CC diagnosis of C. pneumoniae infection in mammals. The nucleic acids
CC and proteins can also be used in the immunization of mammals, the
CC nucleic acids being particularly useful as DNA vaccines for
CC effecting in vivo expression of antigens. The vaccines may also
CC prevent atherosclerosis and bronchial asthma, which are possibly
CC associated with C. pneumoniae.
XX
SQ Sequence 1830 BP; 485 A; 357 C; 443 G; 545 T; 0 other;

Alignment Scores:

Pred. No.:	1.93e-187	Length:	1830
Score:	2603.00	Matches:	532
Percent Similarity:	74.46%	Conservative:	22
Best Local Similarity:	71.51%	Mismatches:	50
Query Match:	60.61%	Indels:	140
DB:	20	Gaps:	8

US-09-830-446-27 (1-841) x AAX06830 (1-1830)

```
Qy         30 LeuSerAlaSerAsnSerPheAspGlyThrThrSerThrThrSerPheSerSerLys--- 48
              |||   :::   :::|||:::::|||   ||||||||||||   |||:::   |||
Db         10 TTAGGGAGTCGTGACAGTTATAATGGTGATACAAGCACCACAGAATTTACTCCTAAAGCG 69

Qy         49 ThrSerSerAlaThrAspGlyThrAsnTyrValPheLysAspSerValValIleGluAsn 68
                 :::|||          ||||||   |||:::          |||   |||
Db         70 GCAACTTCTGATGCTAGTGGCACGACCTATATTCTCGATGGGGATGTCTCGATAAGCCAA 129

Qy         69 ValProLysThrGlyGluThrGlnSerThrSerCysPheLysAsnAspAlaAlaAlaGly 88
                 |||          :::   :::||||||||||||   |||          ||||||
Db        130 GCAGGGAAACAA---ACGAGCTTAACCACAAGTTGTTTTTCTAAC------ACTGCAGGA 180

Qy         89 AspLeuAsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThr 108
              :::|||   |||||||||   |||||||||       |||   ||||||   ::::::|||
Db        181 AATCTTACCTTCTTAGGGAACGGATTTTCTCTTCATTTTGACAATATTATTTCGTCTACT 240

Qy        109 AlaSerGlyAlaAlaIleGlySerGluAlaAlaAsnLysThrValThrLeuSerGlyPhe 128
                 :::|||      :::   :::   ||||||:::                |||||||||
Db        241 GTTGCAGGTGTTGTTGTTAGCAATACAGCAGCTTCTGGGATTACGAAATTCTCAGGATTT 300

Qy        129 SerAlaLeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIle 148
              |||   |||       |||   :::|||   :::|||
Db        301 TCAACTCTTCGGATGCTTGCAGCTCCTAGGACCACA------------------------ 336

Qy        149 AsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsnPhe 168

Db        336 ---------------------------------------------------------- 336

Qy        169 SerThrGlyAspGlyGlyAlaIleAsnCysAlaGlySerLeuLysIleAlaAsnAsnLys 188

Db        336 ---------------------------------------------------------- 336

Qy        189 SerLeuSerPheIleGlyAsnSerSerSerThrArgGlyGlyAlaIleHisThrLysAsn 208

Db        336 ---------------------------------------------------------- 336

Qy        209 LeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAla 228

Db        336 ---------------------------------------------------------- 336
```

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Qy        229 GlyLysGlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSer 248
              ||||||   |||||||||   |||   |||
Db        337 GGTAAA---GGAGCCATTAAAATTACCGATGGT-------------------------- 366

Qy        249 GlyAspIlePheGlu------GlyAsnThrIleGlyAlaThrGlyThrValSerHis 266
                     ::::::||||||      ||||||
Db        367 ------CTGGTGTTTGAGAGTATAGGGAAT---------------------------- 390

Qy        267 SerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyHis 286

Db        390 ------------------------------------------------------------ 390

Qy        287 ThrIleTyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeu 306
                           ||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ------------CTTGATCCGATTACTGTAACAGGATCGACATCTGTTGCTGATGCTCTC 438

Qy        307 AsnIleAsnSerProAspThrGlyAspAsnLysGluTyrThrGlyThrIleValPheSer 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 AATATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACGGGAACCATAGTCTTTTCT 498

Qy        327 GlyGluLysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSerLysLeuLeu 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 GGAGAGAAGCTCACGGAGGCAGAAGCTAAAGATGAGAAGAACCGCACTTCTAAATTACTT 558

Qy        347 GlnAsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAla 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 CAAAATGTTGCTTTTAAAAATGGGACTGTAGTTTTAAAAGGTGATGTCGTTTTAAGTGCG 618

Qy        367 AsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeuVal 386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 AACGGTTTCTCTCAGGATGCAAACTCTAAGTTGATTATGGATTTAGGGACGTCGTTGGTT 678

Qy        387 AlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArgAsn 406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 GCAAACACCGAAAGTATCGAGTTAACGAATTTGGAAATTAATATAGACTCTCTCAGGAAC 738

Qy        407 GlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAspArgPro 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GGGAAAAAGATAAAACTCAGTGCTGCCACAGCTCAGAAAGATATTCGTATAGATCGTCCT 798

Qy        427 ValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeuAsnGluAspHis 446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 GTTGTACTGGCAATTAGCGATGAGAGTTTTTATCAAAATGGCTTTTTGAATGAGGACCAT 858

Qy        447 SerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIleSerAlaAspSer 466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 TCCTATGATGGGATTCTTGAGTTAGATGCTGGGAAAGACATCGTGATTTCTGCAGATTCT 918

Qy        467 ArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGlyLysTrpThrIleAsnTrp 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 CGCAGTATAGATGCTGTACAATCTCCGTATGGCTATCAGGGAAAGTGGACGATCAATTGG 978

Qy        487 SerThrAspAspLysLysAlaThrValSerTrpAlaLysGlnSerPheAsnProThrAla 506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 TCTACTGATGATAAGAAAGCTACGGTTTCTTGGGCGAAGCAGAGTTTTAATCCCACTGCT 1038

Qy        507 GluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySerPheIleAspValArgSer 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 GAGCAGGAGGCTCCGTTAGTTCCTAATCTTCTTTGGGGTTCTTTTATAGATGTTCGTTCC 1098

Qy        527 PheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTyrGluLysArgPheTrpVal 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 TTCCAGAATTTTATAGAGCTAGGTACTGAAGGTGCTCCTTACGAAAAGAGATTTTGGGTT 1158

Qy        547 AlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAsnGlnArgLysPheArgHis 566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GCAGGCATTTCCAATGTTTTGCATAGGAGCGGTCGTGAAAATCAAAGGAAATTCCGTCAT 1218

Qy        567 ValSerGlyGlyAlaValValGlyAlaSerThrArgMetProGlyGlyAspThrLeuSer 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 GTGAGTGGAGGTGCTGTAGTAGGTGCTAGCACGAGGATGCCGGGTGGTGATACCTTGTCT 1278

Qy        587 LeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPheMetAsnThrAsnPheAla 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTGGGTTTTGCTCAGCTCTTTGCGCGTGACAAAGACTACTTTATGAATACCAATTTCGCA 1338

Qy        607 LysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSerLeuTyrSerValValSer 626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 AAGACCTACGCAGGATCTTTACGTTTGCAGCACGATGCTTCCCTATACTCTGTGGTGAGT 1398

Qy        627 IleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuProTyrValSerLysThrLeu 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db       1399 ATCCTTTTAGGAGAGGGAGGACTCCGCGAGATCCTGTTGCCTTATGTTTCCAATACTCTG 1458

Qy        647 ProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAspHisArgMetLysThrGlu 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 CCGTGCTCTTTCTATGGGCAGCTTAGCTACGGCCATACGGATCATCGCATGAAGACCGAG 1518

Qy        667 SerLeuProProProProProThrLeuSerThrAspHisThrSerTrpGlyGlyTyrVal 686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 TCTCTACCCCCCCCCCCCCCGACGCTCTCGACGGATCATACTTCTTGGGGAGGATATGTC 1578

Qy        687 TrpAlaGlyGluLeuGlyThrArgValAlaValGluAsnThrSerGlyArgGlyPhePhe 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1579 TGGGCTGGAGAGCTGGGAACTCGAGTTGCTGTTGAAAATACCAGCGGCAGAGGATTTTTC 1638

Qy        707 GlnGluTyrThrProPheValLysValGlnAlaValTyrAlaArgGlnAspSerPheVal 726
              :::|||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db       1639 CGAGAGTACACTCCATTTGTAAAAGTCCAAGCTGTTTACTCGCGCCAAGATAGCTTTGTT 1698

Qy        727 GluLeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyrAsnLeuAlaIlePro 746
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1699 GAACTAGGAGCTATCAGTCGTGATTTTAGTGATTCGCATCTTTATAACCTTGCGATTCCT 1758

Qy        747 LeuGlyIleLysLeuGluLysArgPheAlaGluGlnTyrTyrHisValValAlaMetTyr 766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1759 CTTGGAATCAAGTTAGAGAAACGGTTTGCAGAGCAATATTATCATGTTGTTGCGATGTAT 1818

Qy        767 SerProAspVal 770
              ||||||||||||
Db       1819 TCTCCAGATGTT 1830
```

RESULT 7
AAA27021
ID AAA27021 standard; DNA; 3000 BP.
XX
AC AAA27021;
XX
DT 11-AUG-2000 (first entry)
XX
DE Chlamydia pneumoniae 98kD putative outer membrane protein gene.
XX
KW Chlamydia; antigen; vaccine; infection; outer membrane protein; ds.
XX
OS Chlamydia pneumoniae.
XX
FH Key   Location/Qualifiers
FT CDS   101..2887
FT   /*tag= a
FT   /product= "98kDa putative outer membrane protein"
XX
PN WO200026237-A2.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-GB03579.
XX
PR 29-OCT-1998; 98US-0106070.
PR 01-MAR-1999; 99US-0122066.
PR 27-OCT-1999; 99US-0428122.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Murdin AD, Oomen RP, Dunn PL;
XX

DR WPI; 2000-365569/31.
DR P-PSDB; AAY94327.
XX
PT Novel Chlamydia 98 kDa putative outer membrane protein antigen, used
PT for vaccination and protection against Chlamydia infection -
XX
PS Claim 1; Fig 1; 93pp; English.
XX
CC The present sequence is the 98kDa putative outer membrane protein gene
CC from Chlamydia pneumoniae. The genomic sequence was amplified using two
CC PCR primers. The 5' primer contains a NotI restriction site, a ribosome
CC binding site, an initiation codon and a sequence close to the 5' end of
CC the 98kDa putative outer membrane protein coding sequence. The 3' primer
CC contains the sequence encoding the C-terminal sequence of the putative
CC outer membrane protein and a BsrG1 restriction site. The stop codon was
CC excluded and an additional nucleotide was inserted to obtain an in-frame
CC C-terminal fusion with the Histidine tag. The PCR product was cloned
CC into a eukaryotic expression vector (pCA-Myc-His) by restricting both
CC the vector and the PCR product with NotI and BamH1 and performing a
CC ligation reaction. This expression vector was injected intramuscularly
CC and intranasally into mice, which were subsequently inoculated with
CC Chlamydia pneumoniae. The chlamydial lung titers of the immunised mice
CC were lower than those of the controls. Thus the 98kDa putative outer
CC membrane protein can be used as a vaccine to provide protection against
CC Chlamydia infections, especially Chlamydia pneumoniae infections.
CC The polypeptide may also be administered orally to treat Chlamydia
CC infection. The present sequence may also be used in the
CC construction of attenuated Chlamydia strains that can over-express the
CC gene or express it in a non-toxic form.
XX
SQ Sequence 3000 BP; 871 A; 617 C; 634 G; 878 T; 0 other;

Alignment Scores:

Pred. No.:	7.75e-110	Length:	3000
Score:	1580.50	Matches:	375
Percent Similarity:	52.54%	Conservative:	121
Best Local Similarity:	39.72%	Mismatches:	306
Query Match:	36.80%	Indels:	142
DB:	21	Gaps:	19

US-09-830-446-27 (1-841) x AAA27021 (1-3000)

```
Qy        15 ThrLeuSerMetSerAsnLeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsn 34
Db       134 ACATTTGCTATTTTCCCTTTGTCTATGATTGCTACCGAGACAGTTTTGGATTCAAGTGCG 193

Qy        35 SerPheAspGlyThrThrSerThrThrSerPheSerSerLysThrSerSerAlaThrAsp 54
Db       194 AGTTTCGATGGG---AATAAAAATGGTAATTTTTCAGTTCGTGAGAGTCAGGAAGATGCT 250

Qy        55 GlyThrAsnTyrValPheLysAspSerValValIleGluAsnValProLysThrGlyGlu 74
Db       251 GGAACTACCTACCTATTTAAGGGAAATGTCACTCTAGAAAATATTCCTGGAACAGGCACA 310

Qy        75 ThrGlnSerThrSerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGly 94
Db       311 GCAATCACAAAAAGCTGTTTTAACAAC------ACTAAGGGCGATTTGACTTTCACAGGT 364

Qy        95 GlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIle 114
Db       365 AACGGGAACTCTCTATTGTTCCAAACGGTGGATGCAGGGACTGTAGCAGGGGCTGCTGTT 424

Qy       115 GlySerGluAlaAlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeu 134
Db       425 AACAGCAGCGTGGTAGATAAATCTACCACGTTTATAGGGTTTTCTTCGCTATCTTTTATT 484

Qy       135 LysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValLys---GlyAsn 153
Db       485 GCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGCCGTTAGCTGCTCTACGGGTAGC 544

Qy       154 LeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsnPheSerThrGlyAspGly 173
Db       545 TTGAGTTTGACAAAAAATGTCAGTTTGCTCTTCAGCAAAAACTTTTCAACGGATAATGGC 604

Qy       174 GlyAlaIleAsnCys---------------------------------------------- 178
Db       605 GGTGCTATCACCGCAAAAACTCTTTCATTAACAGGGACTACAATGTCAGCTCTGTTTTCT 664

Qy       178 ---------------------------------------------------------- 178
Db       665 GAAAATACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTACCATTACT 724

Qy       178 ---------------------------------------------------------- 178
Db       725 GGAAACCAAGGGGAAGTCTCTTTTTCTGACAATACTTCTTCGGATTCTGGAGCTGCAATT 784

Qy       179 ------AlaGlySerLeuLysIleAlaAsnAsnLysSerLeuSerPheIle--------- 193
Db       785 TTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTTCCTTTATTGACAATAAG 844

Qy       193 ---------------------------------------------------------- 193
Db       845 GTCACAGGAGCGAGCTCCTCAACAACGGGGGATATGTCAGGAGGTGCTATCTGTGCTTAT 904

Qy       194 ----------------------------------------------------------Gly 194
Db       905 AAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAGCAAC 964

Qy       195 AsnSerSerSerThrArgGlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGly 214
Db       965 AATACATCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTCCGGA 1024

Qy       215 GlyGluThrLeuPhe----------GlnGlyAsnThrAlaProThrAlaAlaGly 229
Db      1025 GGACTTACCCTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCT---------- 1072

Qy       230 LysGlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGly 249
Db      1073 AAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGGT 1132

Qy       250 AspIleIlePheGluGlyAsnThrIleGlyAlaThr------GlyThrValSerHisSer 267
Db      1133 GACATTGTCTTTTTAGGGAATACAGTCACTTCTACTACTCCTGGGACG---AATAGAAGT 1189

Qy       268 AlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyHisThr 287
Db      1190 AGTATCGACTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTGCTGGTAGAGCC 1249

Qy       288 IleTyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsn 307
Db      1250 ATCTACTTCTATGATCCCATAACTACAGGATCATCCACAACAGTTACAGATGTCTTAAAA 1309

Qy       308 IleAsnSerProAspThrGlyAspAsnLysGluTyrThrGlyThrIleValPheSerGly 327
Db      1310 GTTAATGAGACTCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAGGA 1369

Qy       328 GluLysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSerLysLeuLeuGln 347
Db      1370 GAAAAGTTATCAGAGACAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAG 1429

Qy       348 AsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsn 367
Db      1430 CCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAACATGGAGTGACTCTGCAGACTCAG 1489

Qy       368 GlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeu---Val 386
Db      1490 GCATTCACTCAACAGGCAGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAACCT 1549

Qy       387 AlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArgAsn 406
Db      1550 GCTGATACTAGCACCATA------AACAATTTGGTCATTAACATCAGTTCTATAGACGGT 1603

Qy       407 GlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAspArgPro 426
Db      1604 GCAAAGAAGGCAAAAATAGAAACCAAAGCTACGTCAAAAAATCTGACTTTATCTGGAACC 1663
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```
Qy       427 ValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeuAsnGluAspHis 446
Db      1664 ATCACTTTATTGGACCCGACGGGCACGTTTTATGAAAATCATAGTTTAAGAAATCCTCAG 1723

Qy       447 SerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIleSerAla--AspS 466
Db      1724 TCCTACGAC---ATCTTAGAGCTCAAAGCTTCTGGAACTGTAACAAGCACCGCAGTGACT 1780

Qy       466 erArgSerIleAspAlaValGlnSerPro-TyrGlyTyrGlnGlyLysTrp---ThrIle 484
Db      1781 CCAGATCCTATAATGGGTGAGAAATTCCATTACGGCTATCAGGGAACTTGGGGCCCAATT 1840

Qy       485 AsnTrpSerThrAsp---AspLysLysAlaThrValSerTrpAlaLysGlnSerPheAsn 503
Db      1841 GTTTGGGGGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAAAACTGGCTATATT 1900

Qy       504 ProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySerPheIleAsp 523
Db      1901 CCTAATCCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCATTTATAGAT 1960

Qy       524 ValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTyrGluLysArg 543
Db      1961 ATTAGCTCTCTCCATTATCTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGACCGTGCT 2020

Qy       544 PheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAsnGlnArgLys 563
Db      2021 TTTTGGTGTGCTGGATTATCTAACTTCTTCCATAAGGATAGTACAAAAACACGACGCGGG 2080

Qy       564 PheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArgMetProGlyGlyAsp 583
Db      2081 TTTCGCCATTTGAGTGGCGGTTATGTCATAGGAGGAAACCTACATACTTGTTCAGATAAG 2140

Qy       584 ThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPheMetAsnThr 603
Db      2141 ATTCTTAGTGCTGCATTTTGTCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAG 2200

Qy       604 AsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSerLeuTyrSer 623
Db      2201 AATCAAGGTACAGTCTACGGAGGAACTCTCTATTACCAGCACAACGAAACCTATATCTCT 2260

Qy       624 ValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuProTyrValSer 643
Db      2261 CTTCCTTGC----------------AAACTACGGCCTTGTTCGTTGTCTTATGTTCCT 2302

Qy       644 LysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAspHisArgMet 663
Db      2303 ACAGAGATTCCTGTTCTCTTTTCAGGAAACCTTAGCTACACCCATACGGATAACGATCTG 2362

Qy       664 LysThrGluSerLeuProProProProProThrLeuSerThrAspHisThrSerTrpGly 683
Db      2363 AAAACCAAGTAT--------------ACAACATATCCTACTGTTAAAGGAAGCTGGGGG 2407

Qy       684 GlyTyrValTrpAlaGlyGluLeuGlyThrArg------ValAlaValGluAsnThrSer 701
Db      2408 AATGATAGTTTCGCTTTAGAATTCGGTGGAAGAGCTCCGATTTGCTTAGATGAAAGTGCT 2467

Qy       702 GlyArgGlyPhePheGlnGluTyrThrProPheValLysValGlnAlaValTyrAlaArg 721
Db      2468 ---------CTATTTGAGCAGTACATGCCCTTCATGAAATTGCAGTTTGTCTATGCACAT 2518

Qy       722 GlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyr 741
Db      2519 CAGGAAGGTTTTAAAGAACAGGGAACAGAAGCTCGTGAATTTGGAAGTAGCCGTCTTGTG 2578

Qy       742 AsnLeuAlaIleProLeuGlyIleLysLeuGluLysArg------PheAlaGluGlnTyr 759
Db      2579 AATCTTGCCTTACCTATCGGGATCCGATTTGATAAGGAATCAGACTGCCAAGATGCAACG 2638

Qy       760 TyrHisValValAlaMetTyrSerProAspValCysArgSerAsnProLysCysThrThr 779
Db      2639 TACAATCTAACTCTTGGTTATACTGTGGATCTTGTTCGTAGTAACCCCGACTGTACGACA 2698

Qy       780 ThrLeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAla 799
Db      2699 ACACTGCGAATTAGCGGTGATTCTTGGAAAACCTTCGGTACGAATTTGGCAAGACAAGCT 2758

Qy       800 GlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsn 819
Db      2759 TTAGTCCTTCGTGCAGGGAACCATTTTTGCTTTAACTCAAATTTTGAAGCCTTTAGCCAA 2818

Qy       820 PheGlyPheGluTrpArgGlySerSerArgSerTyrAsnValAspAlaGlySerLysIle 839
Db      2819 TTTTCTTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTAGACTTAGGAGCAAAATAC 2878

Qy       840 LysPhe 841
Db      2879 CAATTC 2884
```

RESULT 8
AAX06820
ID AAX06820 standard; DNA; 2787 BP.
XX
AC AAX06820;
XX
DT 26-APR-1999 (first entry)
XX
DE Chlamydia pneumoniae surface exposed protein Omp8 DNA.
XX
KW Omp8; outer membrane protein 8; surface exposed protein; antigen;
KW infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
XX
OS Chlamydia pneumoniae.
XX
PN WO9858953-A2.
XX
PD 30-DEC-1998.
XX
PF 19-JUN-1998; 98WO-DK00266.
XX
PR 23-JUN-1997; 97DK-0000744.
XX
PA (BIRK/) BIRKELUND S.
PA (CHRI/) CHRISTIANSEN G.
XX
PI Birkelund S, Christiansen G, Knudsen K, Madsen A;
PI Mygind P;
XX
DR WPI; 1999-105610/09.
DR P-PSDB; AAW88421.
XX
PT Species-specific test for identifying mammals infected with
PT Chlamydia pneumoniae - comprises detecting antibodies specific for
PT outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT these proteins
XX
PS Claim 6; Page 52-53; 115pp; English.
XX
CC This DNA sequence codes for the novel 90.0 kDa surface exposed
CC protein Omp8 (see AAW88421) of the human respiratory pathogen
CC Chlamydia pneumoniae. By generating antibodies against C.
CC pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
CC was obtained which reacted with outer membrane proteins. The
CC antibody was used to identify the genes (see AAX06816-27) encoding
CC Omp4-Omp15 proteins (see AAW88417-28) in an expression library of
CC C. pneumoniae DNA. The genes are situated in 2 gene clusters:
CC Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
CC the other, and encode polypeptides of about 89.6-100.3 kDa and
CC about 56.1 kDa. The invention provides a new species specific test
CC for identifying mammals (including humans) infected with Chlamydia
CC pneumoniae. The test comprises detecting antibodies specific for
CC Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC membrane proteins, especially by PCR. The proteins are also used
CC in the diagnosis of C. pneumoniae infection in mammals. The
CC nucleic acids and proteins can also be used in the immunization of
CC mammals, the nucleic acids being particularly useful as DNA
CC vaccines for effecting in vivo expression of antigens. The

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CC   vaccines may also prevent atherosclerosis and bronchial asthma,
CC   which are possibly associated with C. pneumoniae.
XX
SQ   Sequence 2787 BP; 811 A; 583 C; 598 G; 795 T; 0 other;

Alignment Scores:
Pred. No.:              4.79e-109      Length:          2787
Score:                  1569.50        Matches:         373
Percent Similarity:     52.33%         Conservative:    121
Best Local Similarity:  39.51%         Mismatches:      308
Query Match:            36.54%         Indels:          142
DB:                     20             Gaps:            19

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Qy         15 ThrLeuSerMetSerAsnLeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsn 34
Db         34 ACATTTGCTATTTTCCCTTTGTCTATGATTGCTACCGAGACAGTTTTGGATTCAAGTGCG 93

Qy         35 SerPheAspGlyThrThrSerThrThrSerPheSerSerLysThrSerSerAlaThrAsp 54
Db         94 AGTTTCGATGGG---AATAAAAATGGTAATTTTTCAGTTCGTGAGAGTCAGGAAGATGCT 150

Qy         55 GlyThrAsnTyrValPheLysAspSerValValIleGluAsnValProLysThrGlyGlu 74
Db        151 GGAACTACCTACCTATTTAAGGGAAATGTCACTCTAGAAAATATTCCTGGAACAGGCACA 210

Qy         75 ThrGlnSerThrSerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGly 94
Db        211 GCAATCACAAAAAGCTGTTTTAACAAC------ACTAAGGGCGATTTGACTTTCACAGGT 264

Qy         95 GlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIle 114
Db        265 AACGGGAACTCTCTATTGTTCCAAACGGTGGATGCAGGGACTGTAGCAGGGGCTGCTGTT 324

Qy        115 GlySerGluAlaAlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeu 134
Db        325 AACAGCAGCGTGGTAGATAAATCTACCACGTTTATAGGGTTTTCTTCGCTATCTTTTATT 384

Qy        135 LysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValLys---GlyAsn 153
Db        385 GCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGCCGTTAGCTGCTCTACGGGTAGC 444

Qy        154 LeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsnPheSerThrGlyAspGly 173
Db        445 TTGAAGTTTGACAAAAATGTCAGTTTGCTCTTCAGCAAAAACTTTTCAACGGATAATGGC 504

Qy        174 GlyAlaIleAsnCys---------------------------------------------- 178
Db        505 GGTGCTATCACCGCAAAAACTCTTTCATTAACAGGGACTACAATGTCAGCTCTGTTTTCT 564

Qy        178 ---------------------------------------------------------- 178
Db        565 GAAAATACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTACCATTACT 624

Qy        178 ---------------------------------------------------------- 178
Db        625 GGAAACCAAGGGGAAGTCTCTTTTTCTGACAATACTTCTTCGGATTCTGGAGCTGCAATT 684

Qy        179 ------AlaGlySerLeuLysIleAlaAsnAsnLysSerLeuSerPheIle--------- 193
Db        685 TTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTTCCTTTATTGACAATAAG 744

Qy        193 ---------------------------------------------------------- 193
Db        745 GTCACAGGAGCGAGCTCCTCAACAACGGGGGATATGTCAGGAGGTGCTATCTGTGCTTAT 804

Qy        194 ----------------------------------------------------------Gly 194
Db        805 AAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAGCAAC 864

Qy        195 AsnSerSerSerThrArgGlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGly 214
Db        865 AATACATCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTCCGGA 924

Qy        215 GlyGluThrLeuPhe--------------GlnGlyAsnThrAlaProThrAlaAlaGly 229
Db        925 GGACTTACCCTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCT------------ 972

Qy        230 LysGlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGly 249
Db        973 AAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGGT 1032

Qy        250 AspIleIlePheGluGlyAsnThrIleGlyAlaThr------GlyThrValSerHisSer 267
Db       1033 GACATTGTCTTTTTAGGGAATACAGTCACTTCTACTACTCCTGGGACG---AATAGAAGT 1089

Qy        268 AlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyHisThr 287
Db       1090 AGTATCGACTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTGCTGGTAGAGCC 1149

Qy        288 IleTyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsn 307
Db       1150 ATCTACTTCTATGATCCCATAACTACAGGATCTTCCACAACAGTTACAGATGTCTTAAAA 1209

Qy        308 IleAsnSerProAspThrGlyAspAsnLysGluTyrThrGlyThrIleValPheSerGly 327
Db       1210 GTTAATGAGACTCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAGGA 1269

Qy        328 GluLysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSerLysLeuLeuGln 347
Db       1270 GAAAAGTTATCAGAGACAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAG 1329

Qy        348 AsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsn 367
Db       1330 CCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAACATGGAGTGACTCTGCAGACTCAG 1389

Qy        368 GlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeu---Val 386
Db       1390 GCATTCACTCAACAGGCAGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAACCT 1449

Qy        387 AlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArgAsn 406
Db       1450 GCTGATACTAGCACCATA------AACAATTTGGTCATTAACATCAGTTCTATAGACGGT 1503

Qy        407 GlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAspArgPro 426
Db       1504 GCAAAGAAGGCAAAAATAGAAACCAAAGCTACGTCAAAAAATCTGACTTTATCTGGAACC 1563

Qy        427 ValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeuAsnGluAspHis 446
Db       1564 ATCACTTTATTGGACCCGACGGGCACGTTTTATGAAAATCATAGTTTAAGAAATCCTCAG 1623

Qy        447 SerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIleSerAla--AspS 466
Db       1624 TCCTACGAC---ATCTTAGAGCTCAAAGCTTCTGGAACTGTAACAAGCACCGCAGTGACT 1680

Qy        466 erArgSerIleAspAlaValGlnSerPro-TyrGlyTyrGlnGlyLysTrp---ThrIle 484
Db       1681 CCAGATCCTATAATGGGTGAGAAATTCCATTACGGCTATCAGGGAACTTGGGGCCCAATT 1740

Qy        485 AsnTrpSerThrAsp---AspLysLysAlaThrValSerTrpAlaLysGlnSerPheAsn 503
Db       1741 GTTTGGGGGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAAAACTGGCTATATT 1800

Qy        504 ProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySerPheIleAsp 523
Db       1801 CCTAATCCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCATTTATAGAT 1860

Qy        524 ValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTyrGluLysArg 543
Db       1861 ATTAGCTCTCTCCATTATCTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGACCGTGCT 1920

Qy        544 PheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAsnGlnArgLys 563
Db       1921 TTTTGGTGTGCTGGATTATCTAACTTCTTCCATAAGGATAGTACAAAAACACGACGCGGG 1980
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Qy        564 PheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArgMetProGlyGlyAsp 583
              ||||||||||:::|||||||||   |||:::|||   :::
Db       1981 TTTCGCCATTTGAGTGGCGGTTATGTCATAGGAGGAAACCTACATACTTGTTCAGATAAG 2040

Qy        584 ThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPheMetAsnThr 603
              ||||||      |||   |||||||||   ||||||:::||||||||||:::
Db       2041 ATTCTTAGTGCTGCATTTTGTCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAG 2100

Qy        604 AsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSerLeuTyrSer 623
              |||           |||  |||:::|||      ||||||:::   :::      |||
Db       2101 AATCAAGGTACAGTCTACGGAGGAACTCTCTATTACCAGCACAACGAAACCTATATCTCT 2160

Qy        624 ValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuProTyrValSer 643
              :::                          ||||||          |||   ||||||
Db       2161 CTTCCTTGC-----------------AAACTACGGCCTTGTTCGTTGTCTTATGTTCCT 2202

Qy        644 LysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAspHisArgMet 663
              :::|||      |||  |||  |||||||||  ||||||||:::   :::
Db       2203 ACAGAGATTCCTGTTCTCTTTTCAGGAAACCTTAGCTACACCCATACGGATAACGATCTG 2262

Qy        664 LysThrGluSerLeuProProProProProThrLeuSerThrAspHisThrSerTrpGly 683
              ||||||:::                    |||      |||          |||||||||
Db       2263 AAAACCAAGTAT--------------ACAACATATCCTACTGTTAAAGGAAGCTGGGGG 2307

Qy        684 GlyTyrValTrpAlaGlyGluLeuGlyThrArg------ValAlaValGluAsnThrSer 701
                 :::|||   |||   |||   |||      :::   ::::::   ::::::
Db       2308 AATGATAGTTTCGCTTTAGAATTCGGTGGAAGAGCTCCGATTTGCTTAGATGAAAGTGCT 2367

Qy        702 GlyArgGlyPhePheGlnGluTyrThrProPheValLysValGlnAlaValTyrAlaArg 721
                    |||:::::::|||   ||||||:::|||:::|||   |||||||||
Db       2368 ---------CTATTTGAGCAGTACATGCCCTTCATGAAATTGCAGTTTGTCTATGCACAT 2418

Qy        722 GlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyr 741
              |||:::   |||   |||   |||       :::|||:::|||       |||   |||
Db       2419 CAGGAAGGTTTTAAAGAACAGGGAACAGAAGCTCGTGAATTTGGAAGTAGCCGTCTTGTG 2478

Qy        742 AsnLeuAlaIleProLeuGlyIleLysLeuGluLysArg------PheAlaGluGlnTyr 759
              |||||||||:::|||:::||||||:::   :::|||                  :::
Db       2479 AATCTTGCCTTACCTATCGGGATCCGATTTGATAAGGAATCAGACTGCCAAGATGCAACG 2538

Qy        760 TyrHisValValAlaMetTyrSerProAspValCysArgSerAsnProLysCysThrThr 779
              |||::::::      |||:::   |||:::   ||||||||||||   |||||||||
Db       2539 TACAATCTAACTCTTGGTTATACTGTGGATCTTGTTCGTAGTAACCCCGACTGTACGACA 2598

Qy        780 ThrLeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAla 799
              ||||||      :::      ||||||||||||   |||:::||||||||||||||||||
Db       2599 ACACTGCGAATTAGCGGTGATTCTTGGAAAACCTTCGGTACGAATTTGGCAAGACAAGCT 2658

Qy        800 GlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsn 819
                 :::::::::|||                  :::      |||   |||
Db       2659 TTAGTCCTTCGTGCAGGGAACCATTTTTGCTTTAACTCAAATTTTGAAGCCTTTAGCCAA 2718

Qy        820 PheGlyPheGluTrpArgGlySerSerArgSerTyrAsnValAspAlaGlySerLysIle 839
              |||   ||||||   ||||||||||||||:::||||||||||||   |||:::|||
Db       2719 TTTTCTTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTAGACTTAGGAGCAAAATAC 2778

Qy        840 LysPhe 841
              :::|||
Db       2779 CAATTC 2784

RESULT 9
ABQ84758
ID   ABQ84758 standard; DNA; 2520 BP.
XX
AC   ABQ84758;
XX
DT   25-FEB-2003  (first entry)
XX
DE   Chlamydia psittaci antigen CP4#4 encoding DNA SEQ ID NO:22.
XX
KW   Chlamydia psittaci; vaccination; vaccine; antigen; immune response;
KW   immunisation; antibacterial; infection; gene; ds.
XX
OS   Chlamydia psittaci.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..2520
FT                   /*tag=  a
FT                   /product= "antigen CP4#4"
XX
PN   WO200253588-A2.
XX
PD   11-JUL-2002.
XX
PF   17-DEC-2001; 2001WO-US48715.
XX
PR   15-DEC-2000; 2000US-0738269.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Johnston SA,  Stemke-Hale K,  Sykes KF,  Kaltenboeck B;
XX
DR   WPI; 2002-537942/57.
DR   P-PSDB; ABP56002.
XX
PT   Vaccine for immunization of animal, preferably bovine, against
PT   Chlamydia psittaci, comprises at least one polynucleotide having a C.
PT   psittaci sequence, or at least one C. psittaci antigen  -
XX
PS   Claim 14; Page 126; 164pp; English.
XX
CC   The present invention describes a vaccine (I) for the immunisation of an
CC   animal against Chlamydia psittaci comprising at least one polynucleotide
CC   (Ia) having a C. psittaci sequence, or at least one C. psittaci antigen
CC   (Ib), and a carrier. (Ia) and (Ib) have antibacterial activity. (I) is
CC   useful for the immunisation of a bovine. The present sequence encodes a
CC   C. psittaci antigen from the present invention.
XX
SQ   Sequence 2520 BP; 774 A; 584 C; 490 G; 672 T; 0 other;

Alignment Scores:
Pred. No.:                1.29e-103      Length:          2520
Score:                    1497.00        Matches:         357
Percent Similarity:       56.21%         Conservative:    132
Best Local Similarity:    41.03%         Mismatches:      321
Query Match:              34.85%         Indels:          60
DB:                       24             Gaps:            25

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Qy          1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
              ||||||   |||:::   :::   |||||||||         :::|||      ||||||
Db          1 ATGAAACATCCAGTCTACTGGTTCTTAATATCC------TCGAGCCTATTTGCCTCGAAT 54

Qy         21 LeuLeuGlyAlaAlaThrThrGluGlu------LeuSerAlaSerAsnSerPheAspGly 38
                 |||      |||         :::      |||:::   |||:::|||::::::|||
Db         55 TCTTTGAGCTTCGCTAACGACGCTCAAACAGCCTTAACTCCCTCCGATAGCTATAATGGA 114

Qy         39 ThrThrSerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyr 58
                 ::::::      |||      |||   :::|||:::      ||||||   |||
Db        115 AATGTGACCTCTGAGGAGTTCCAGGTAAAAGAAACTTCATCA------GGAACAACGTAT 168

Qy         59 ValPheLysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThr 78
                 :::   :::|||   |||            |||            :::
Db        169 ACTTGTGAAGGCAATGTGTGTATCTCCTTTGCAGGGAAAGATTCAGGTCTAAAGAAA--- 225

Qy         79 SerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSer 98
              |||||||||      :::|||      :::|||   |||||||||   |||::::::
Db        226 AGTTGTTTC---------TCAGCTACTGATAACCTTACCTTCCTAGGAAACGGGTATACT 276

Qy         99 PheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAla 118
                 |||   ||||||      |||   ::::::      ||||||      :::
Db        277 CTTTGCTTTGATAATATTACTACTACAGCTAGTAACCCCGGAGCCATTAATGTTCAAGGT 336

Qy        119 AlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAla 138
```


Db 337 CAAGGAAAAACCTTAGGCATCTCAGGATTTTCTTTATTTTCATGTGCTTATTGTCCTCCA 396
Qy 139 SerThrValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAsp 158
Db 397 GGC------ACAACTGGTTACGGAGCTATACAGACTAAAGGCAACACAACTTTAAAAGAT 450
Qy 159 AsnAspLysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCys 178
Db 451 AACTCTAGTCTTGTCTTCCATAAAAACTGCTCAACAGCAGAAGGTGGGGCTATCCAGTGT 510
Qy 179 AlaGlySer----------LeuLysIleAlaAsnAsnLysSerLeuSerPheIleGly 194
Db 511 AAAGGAAGCAGTGATGCTGAATTAAAAATAGAAAATAATCAGAATCTGGTTTTCTCAGAA 570
Qy 195 AsnSerSerSerThrArgGlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGly 214
Db 571 AACTCCTCCACTTCAAAAGGCGGGGCTATTTATGCTGATAAACTCACCATTGTCTCAGGT 630
Qy 215 GlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGly---LysGlyGlyAla 233
Db 631 GGGCCTACATTATTTTCTAACAACTCTGTATCCAACGGTTCATCCCCTAAAGGCGGAGCT 690
Qy 234 IleAlaIleAlaAsp---SerGlyThrLeuSerIleSerGlyAspSerGlyAspIleIle 252
Db 691 ATTAGCATAAAAGATTCAAGTGGTGAATGTAGCCTAACCGCTGATCTCGGAGATATTACC 750
Qy 253 PheGluGlyAsn----------ThrIleGlyAlaThrGlyThrValSerHisSerAla 268
Db 751 TTCGATGGGAACAAAATCATCAAAACTAGTGGTGGAAGTTCTACAGTAACAAGAAATTCC 810
Qy 269 IleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyHisThrIle 288
Db 811 ATAGATCTCGGCACA---GGGAAATTTACAAAGCTACGTGCTAAAGACGGCTTCGGAATT 867
Qy 289 TyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsnIle 308
Db 868 TTCTTCTATGACCCTATTACTGGGGGAGGATCT----------GATGAACTAAACATT 915
Qy 309 AsnSerProAspThrGlyAspAsnLysGluTyrThrGlyThrIleValPheSerGlyGlu 328
Db 916 AATAAAAAAGAAACTGTTGAT---------TATACAGGAAAGATCGTCTTCTCAGGTGAA 966
Qy 329 LysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSerLysLeuLeuGlnAsn 348
Db 967 AAATTATCCGATGAAGAAAAAGCACGAGCGGAAAACCTAGCTTCTACTTTCAACCAACCC 1026
Qy 349 ValAlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsnGly 368
Db 1027 ATCACATTATCAGCAGGATCTCTTGTACTTAAAGATGGTGTATCTGTAACCGCAAAACAA 1086
Qy 369 PheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeu--------- 385
Db 1087 GTAACGCAGGAAGCGGGATCTACCGTTGTCATGGATCTAGGGACCACATTACAGACGCCT 1146
Qy 386 ValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArg 405
Db 1147 TCTTCAGGTGGAGAAACCATCACCCTAACTAATCTAGATATTAACATCGCCTCGTTGGGG 1206
Qy 406 AsnGly---------LysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArg 422
Db 1207 GGGGGGGGGGTACCTCTCCTGCTAAACTCGCAACAAATACAGCAAGTCAAGCTATAACT 1266
Qy 423 IleAspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeu 442
Db 1267 ATTAAC---GCTGTCAATCTAGTCGATGCTGATGGCAATGCTTATGAAGATCCTATTCTT 1323
Qy 443 AsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIle 462
Db 1324 GCTACGTCTAAACCTTTCACAGCAATAGTAGCTACAACTAACGCTAGTACAGTCACACAG 1383
Qy 463 SerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGlyLysTrp 482
Db 1384 CCTACAGATAATCTAACAAATTATGTCCCTCCTACTCATTACGGTTACCAAGGAAATTGG 1443
Qy 483 ThrIleAsnTrpSerThrAsp------AspLysLysAlaThrValSerTrpAlaLysGln 500
Db 1444 ACAGTAACTTGGGACACCGAAACAGCTACAAAAACAGCCACTCTAACTTGGGAACAAACT 1503
Qy 501 SerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySer 520
Db 1504 GGCTACTCCCCTAACCCAGAACGTCAAGGACCTTTAGTCCCGAATACTCTTTGGGGTGCA 1563
Qy 521 PheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTyr 540
Db 1564 TTCTCTGACCTCAGAGCTATACAAAACTTAATGGATATTAGCGTCAATGGCGCTGACTAC 1623
Qy 541 GluLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAsn 560
Db 1624 CATAGAGGTTTTTGGGTATCCGGTCTAGCTAACTTCTTACACAAAAGTGGCTCTGATACT 1683
Qy 561 GlnArgLysPheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArgMetPro 580
Db 1684 AAACGCAAGTTCCGTCACAATAGCGCCGGATACGCTTTAGGCGTCTACGCAAAAACTCCT 1743
Qy 581 GlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPhe 600
Db 1744 TCTGATGATATTTTCAGTGCGGCTTTCTGCCAACTCTTCGGAAAGGACAAAGACTATTTA 1803
Qy 601 MetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSer 620
Db 1804 GTGTCGAAAAACAACGCCAACATTTACGCAGGTTCTCTCTATTATCAGCAT---ATCTCC 1860
Qy 621 LeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuPro 640
Db 1861 TATTGGAGC--------------------------GCTTGGCAGAATCTGCTACAAAAC 1893
Qy 641 TyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAsp 660
Db 1894 ACTATCGGTGCAGAAGCTCCGTTAGTCCTTAACGCACAGTTAACTTATTGTCATGCTTCA 1953
Qy 661 HisArgMetLysThrGlu---------SerLeuProProProProProThrLeuSerThr 677
Db 1954 AACGACATGAAAACCAACATGACGACTACTTACGCTCCTCGTAAAACAACGTATGCAGAA 2013
Qy 678 AspHisThrSerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAlaVal 697
Db 2014 ATCAAGGGTGATTGGGGTAACGATTGTTTCGGAGTCGAGCTTGGTGCAACTGTGCCTATC 2073
Qy 698 GluAsnThrSerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGlnAla 717
Db 2074 CAAACAGAATCTTCTCTC---CTATTCGATATGTACTCACCTTTCCTGAAGTTTCAACTT 2130
Qy 718 ValTyrAlaArgGlnAspSerPheValGluLeuGlyAla---IleSerArgAspPheSer 736
Db 2131 GTGCATACGCACCAAGATGACTTTAAGGAAAACAATAGCGATCAGGGAAGATACTTCGAA 2190
Qy 737 AspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPheAla 756
Db 2191 AGCAGCAATCTCACCAACCTTTCTCTGCCTATCGGCATCAAGTTTGAG---AGATTTGCT 2247
Qy 757 GluGln---------TyrTyrHisValValAlaMetTyrSerProAspValCysArgSer 773
Db 2248 AACAACGATACAGCTTCTTATCATGTCACTGCTGCTTATTCTCCTGATATCGTAAGAAGT 2307
Qy 774 AsnProLysCysThrThrThrLeuLeuSerAsnGlnGlySer------TrpLysThrLys 791
Db 2308 AACCCTGACTGTACTACTTCTCTGTTAGTAAGCCCCGACTCTGCTGTCTGGGTAACGAAA 2367
Qy 792 GlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGly 811
Db 2368 GCCAACAACCTTGCGCGAAGCGCCTTCATGCTACAAGCAGGAAACTACTTGTCTTTAAGT 2427
Qy 812 AlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArgSerTyr 831
Db 2428 CACAACATAGAAATCTTCAGCCAGTTCGGTTTCGAGCTCAGGGGATCTTCACGAACCTAT 2487

```
Qy        832 AsnValAspAlaGlySerLysIleLysPhe 841
              |||||||||   |||||||||||||:::|||
Db       2488 AACGTAGATCTCGGATCGAAGATCCAGTTC 2517

RESULT 10
ABQ78016
ID   ABQ78016 standard; DNA; 2520 BP.
XX
AC   ABQ78016;
XX
DT   03-OCT-2002  (first entry)
XX
DE   Chlamydia polynucleotide SEQ ID NO 22.
XX
KW   Chlamydia; antibacterial; vaccine; immune response; infection; gene; ds.
XX
OS   Chlamydia psittaci.
XX
PN   WO200247718-A2.
XX
PD   20-JUN-2002.
XX
PF   17-DEC-2001; 2001WO-US48773.
XX
PR   15-DEC-2000; 2000US-255839P.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Johnston SA;
XX
DR   WPI; 2002-583472/62.
DR   P-PSDB; ABB98211.
XX
PT   Vaccine useful for immunizing an animal, comprising at least one
PT   polynucleotide having a Chlamydia sequence or at least one Chlamydia
PT   antigen  -
XX
PS   Claim 6; Page 133-134; 183pp; English.
XX
CC   The invention relates to a vaccine (I) comprising at least one
CC   polynucleotide (ABQ78008-ABQ78039) having a Chlamydia sequence or at
CC   least one Chlamydia antigen (ABB98203-ABB98234) and a pharmaceutically
CC   acceptable carrier. The antigens are useful for immunising an animal, by
CC   providing at least one Chlamydia antigen or its antigenic fragment to the
CC   animal, in an amount effective to induce an immune response in the animal
CC   e.g. mammals including bovine or human. The method is effective to induce
CC   an immune response against C. psittaci, C. pneumoniae or non-Chlamydia
CC   infection. The method further involves administering to the animal an
CC   antigen or an antigenic fragment from Chlamydia species other than
CC   C. psittaci or C. pneumoniae or an antigenic fragment from a
CC   non-Chlamydia species.
XX
SQ   Sequence 2520 BP; 774 A; 584 C; 490 G; 672 T; 0 other;

Alignment Scores:
Pred. No.:              1.29e-103      Length:          2520
Score:                  1497.00        Matches:         357
Percent Similarity:     56.21%         Conservative:    132
Best Local Similarity:  41.03%         Mismatches:      321
Query Match:            34.85%         Indels:          60
DB:                     24             Gaps:            25

US-09-830-446-27 (1-841) x ABQ78016 (1-2520)

Qy          1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
              ||||||   |||:::   :::   |||||||||         :::|||      ||||||
Db          1 ATGAAACATCCAGTCTACTGGTTCTTAATATCC------TCGAGCCTATTTGCCTCGAAT 54

Qy         21 LeuLeuGlyAlaAlaThrThrGluGlu------LeuSerAlaSerAsnSerPheAspGly 38
                |||      |||          :::      |||:::   |||:::|||::::::|||
Db         55 TCTTTGAGCTTCGCTAACGACGCTCAAACAGCCTTAACTCCCTCCGATAGCTATAATGGA 114

Qy         39 ThrThrSerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyr 58
              :::::      |||      |||   :::|||:::      ||||||   |||
Db        115 AATGTGACCTCTGAGGAGTTCCAGGTAAAAGAAACTTCATCA------GGAACAACGTAT 168

Qy         59 ValPheLysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThr 78
              :::   :::|||   |||              |||             :::
Db        169 ACTTGTGAAGGCAATGTGTGTATCTCCTTTGCAGGGAAAGATTCAGGTCTAAAGAAA--- 225

Qy         79 SerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSer 98
              ||||||||        :::|||      :::|||   ||||||||   |||::::::
Db        226 AGTTGTTTC---------TCAGCTACTGATAACCTTACCTTCCTAGGAAACGGGTATACT 276

Qy         99 PheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAla 118
              |||   ||||||      |||   ::::::      ||||||      :::
Db        277 CTTTGCTTTGATAATATTACTACTACAGCTAGTAACCCCGGAGCCATTAATGTTCAAGGT 336

Qy        119 AlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAla 138
              ||||||:::   :::|||||||||||||      |||             |||
Db        337 CAAGGAAAAACCTTAGGCATCTCAGGATTTTCTTTATTTTCATGTGCTTATTGTCCTCCA 396

Qy        139 SerThrValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAsp 158
              |||   |||   |||||||||      |||||||||   :::|||   |||
Db        397 GGC------ACAACTGGTTACGGAGCTATACAGACTAAAGGCAACACAACTTTAAAAGAT 450

Qy        159 AsnAspLysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCys 178
              |||      ::::::      |||   ||||||   :::||||||||||||   |||
Db        451 AACTCTAGTCTTGTCTTCCATAAAAACTGCTCAACAGCAGAAGGTGGGGCTATCCAGTGT 510

Qy        179 AlaGlySer-----------LeuLysIleAlaAsnAsnLysSerLeuSerPheIleGly 194
              ||||||             |||||||||   ||||||::::::|||   |||
Db        511 AAAGGAAGCAGTGATGCTGAATTAAAAATAGAAAATAATCAGAATCTGGTTTTCTCAGAA 570

Qy        195 AsnSerSerSerThrArgGlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGly 214
              |||||||||:::::::::||||||||||||:::      ||||||:::   ||||||
Db        571 AACTCCTCCACTTCAAAAGGCGGGGCTATTTATGCTGATAAACTCACCATTGTCTCAGGT 630

Qy        215 GlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGly---LysGlyGlyAla 233
              |||   |||||||||      |||:::             :::      ||||||||||||
Db        631 GGGCCTACATTATTTTCTAACAACTCTGTATCCAACGGTTCATCCCCTAAAGGCGGAGCT 690

Qy        234 IleAlaIleAlaAsp---SerGlyThrLeuSerIleSerGlyAspSerGlyAspIleIle 252
              |||:::|||   |||   ||||||      |||::::::   |||   |||||||||
Db        691 ATTAGCATAAAAGATTCAAGTGGTGAATGTAGCCTAACCGCTGATCTCGGAGATATTACC 750

Qy        253 PheGluGlyAsn-----------ThrIleGlyAlaThrGlyThrValSerHisSerAla 268
              |||:::||||||            |||   |||   :::   ||||||:::   ::::::
Db        751 TTCGATGGGAACAAAATCATCAAAACTAGTGGTGGAAGTTCTACAGTAACAAGAAATTCC 810

Qy        269 IleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyHisThrIle 288
              ||||||||||||||      |||   |||   |||||||||      |||   |||
Db        811 ATAGATCTCGGCACA---GGGAAATTTACAAAGCTACGTGCTAAAGACGGCTTCGGAATT 867

Qy        289 TyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsnIle 308
              :::||||||||||||||||      ||||||            |||   |||||||||
Db        868 TTCTTCTATGACCCTATTACTGGGGGAGGATCT-----------GATGAACTAAACATT 915

Qy        309 AsnSerProAspThrGlyAspAsnLysGluTyrThrGlyThrIleValPheSerGlyGlu 328
              |||      :::|||   |||         ||||||||   ||||||||||||||||||
Db        916 AATAAAAAAGAAACTGTTGAT---------TATACAGGAAAGATCGTCTTCTCAGGTGAA 966

Qy        329 LysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSerLysLeuLeuGlnAsn 348
              ||||||:::::   |||          :::|||      |||          |||
Db        967 AAATTATCCGATGAAGAAAAAGCACGAGCGGAAAACCTAGCTTCTACTTTCAACCAACCC 1026

Qy        349 ValAlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsnGly 368
              :::          |||::::::|||||||||      |||   :::::::|||
Db       1027 ATCACATTATCAGCAGGATCTCTTGTACTTAAAGATGGTGTATCTGTAACCGCAAAACAA 1086

Qy        369 PheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeu--------- 385
                :::|||:::|||   |||   ::::::|||||||||||||||:::|||
Db       1087 GTAACGCAGGAAGCGGGATCTACCGTTGTCATGGATCTAGGGACCACATTACAGACGCCT 1146

Qy        386 ValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArg 405
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Db       1147 TCTTCAGGTGGAGAAACCATCACCCTAACTAATCTAGATATTAACATCGCCTCGTTGGGG 1206

Qy        406 AsnGly---------LysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArg 422

Db       1207 GGGGGGGGGGGTACCTCTCCTGCTAAACTCGCAACAAATACAGCAAGTCAAGCTATAACT 1266

Qy        423 IleAspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeu 442

Db       1267 ATTAAC---GCTGTCAATCTAGTCGATGCTGATGGCAATGCTTATGAAGATCCTATTCTT 1323

Qy        443 AsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIle 462

Db       1324 GCTACGTCTAAACCTTTCACAGCAATAGTAGCTACAACTAACGCTAGTACAGTCACACAG 1383

Qy        463 SerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGlyLysTrp 482

Db       1384 CCTACAGATAATCTAACAAATTATGTCCCTCCTACTCATTACGGTTACCAAGGAAATTGG 1443

Qy        483 ThrIleAsnTrpSerThrAsp------AspLysLysAlaThrValSerTrpAlaLysGln 500

Db       1444 ACAGTAACTTGGGACACCGAAACAGCTACAAAAACAGCCACTCTAACTTGGGAACAAACT 1503

Qy        501 SerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySer 520

Db       1504 GGCTACTCCCCTAACCCAGAACGTCAAGGACCTTTAGTCCCGAATACTCTTTGGGGTGCA 1563

Qy        521 PheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTyr 540

Db       1564 TTCTCTGACCTCAGAGCTATACAAAACTTAATGGATATTAGCGTCAATGGCGCTGACTAC 1623

Qy        541 GluLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAsn 560

Db       1624 CATAGAGGTTTTTGGGTATCCGGTCTAGCTAACTTCTTACACAAAAGTGGCTCTGATACT 1683

Qy        561 GlnArgLysPheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArgMetPro 580

Db       1684 AAACGCAAGTTCCGTCACAATAGCGCCGGATACGCTTTAGGCGTCTACGCAAAAACTCCT 1743

Qy        581 GlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPhe 600

Db       1744 TCTGATGATATTTTCAGTGCGGCTTTCTGCCAACTCTTCGGAAAGGACAAAGACTATTTA 1803

Qy        601 MetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSer 620

Db       1804 GTGTCGAAAAACAACGCCAACATTTACGCAGGTTCTCTCTATTATCAGCAT---ATCTCC 1860

Qy        621 LeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuPro 640

Db       1861 TATTGGAGC-------------------------GCTTGGCAGAATCTGCTACAAAAC 1893

Qy        641 TyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAsp 660

Db       1894 ACTATCGGTGCAGAAGCTCCGTTAGTCCTTAACGCACAGTTAACTTATTGTCATGCTTCA 1953

Qy        661 HisArgMetLysThrGlu---------SerLeuProProProProProThrLeuSerThr 677

Db       1954 AACGACATGAAAACCAACATGACGACTACTTACGCTCCTCGTAAAACAACGTATGCAGAA 2013

Qy        678 AspHisThrSerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAlaVal 697

Db       2014 ATCAAGGGTGATTGGGGTAACGATTGTTTCGGAGTCGAGCTTGGTGCAACTGTGCCTATC 2073

Qy        698 GluAsnThrSerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGlnAla 717

Db       2074 CAAACAGAATCTTCTCTC---CTATTCGATATGTACTCACCTTTCCTGAAGTTTCAACTT 2130

Qy        718 ValTyrAlaArgGlnAspSerPheValGluLeuGlyAla---IleSerArgAspPheSer 736

Db       2131 GTGCATACGCACCAAGATGACTTTAAGGAAAACAATAGCGATCAGGGAAGATACTTCGAA 2190

Qy        737 AspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPheAla 756

Db       2191 AGCAGCAATCTCACCAACCTTTCTCTGCCTATCGGCATCAAGTTTGAG---AGATTTGCT 2247

Qy        757 GluGln---------TyrTyrHisValValAlaMetTyrSerProAspValCysArgSer 773

Db       2248 AACAACGATACAGCTTCTTATCATGTCACTGCTGCTTATTCTCCTGATATCGTAAGAAGT 2307

Qy        774 AsnProLysCysThrThrThrLeuLeuSerAsnGlnGlySer------TrpLysThrLys 791

Db       2308 AACCCTGACTGTACTACTTCTCTGTTAGTAAGCCCCGACTCTGCTGTCTGGGTAACGAAA 2367

Qy        792 GlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGly 811

Db       2368 GCCAACAACCTTGCGCGAAGCGCCTTCATGCTACAAGCAGGAAACTACTTGTCTTTAAGT 2427

Qy        812 AlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArgSerTyr 831

Db       2428 CACAACATAGAAATCTTCAGCCAGTTCGGTTTCGAGCTCAGGGGATCTTCACGAACCTAT 2487

Qy        832 AsnValAspAlaGlySerLysIleLysPhe 841

Db       2488 AACGTAGATCTCGGATCGAAGATCCAGTTC 2517
```

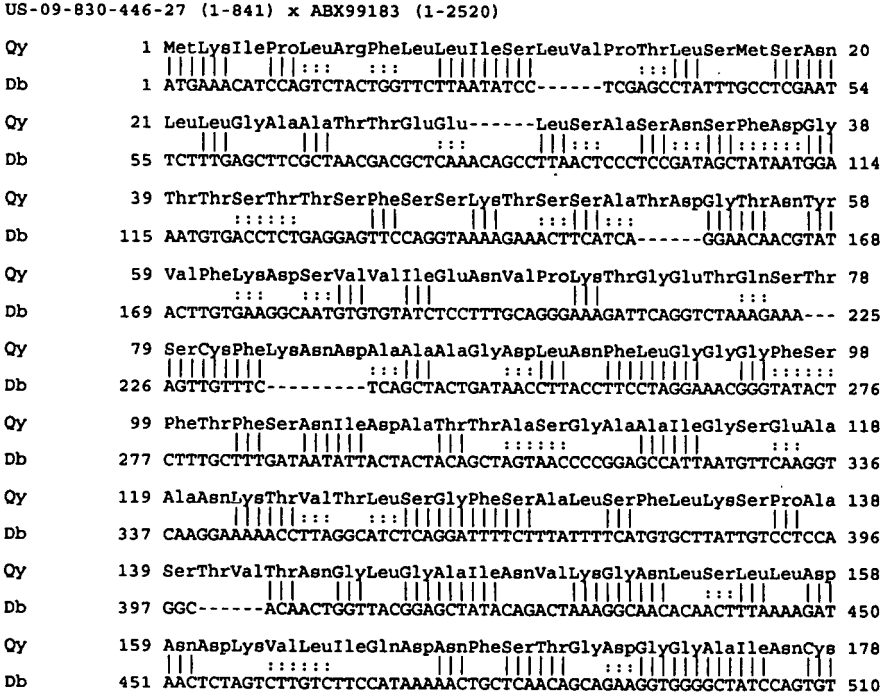
RESULT 11
ABX99183
ID ABX99183 standard; DNA; 2520 BP.
XX
AC ABX99183;
XX
DT 20-MAY-2003 (first entry)
XX
DE C. psittaci genomic DNA sequence CP4 #4 #2.
XX
KW DNA vaccine; chlamydia infection; blindness; mastitis; infertility;
KW abortion; sexually transmitted disease; atherosclerotic plaque; ds;
KW community-acquired pneumonia; coronary heart disease.
XX
OS Chlamydia psittaci.
XX
PN US2002183272-A1.
XX
PD 05-DEC-2002.
XX
PF 17-DEC-2001; 2001US-0023437.
XX
PR 16-AUG-2000; 2000US-225839P.
XX
PA (JOHN/) JOHNSTON S A.
PA (STEM/) STEMKE-HALE K.
PA (SYKE/) SYKES K F.
PA (KALT/) KALTENBOECK B.
XX
PI Johnston SA, Stemke-Hale K, Sykes KF, Kaltenboeck B;
XX
DR WPI; 2003-328634/31.
DR P-PSDB; ABU66267.
XX
PT New vaccine comprising a polynucleotide with a Chlamydia sequence or a
PT Chlamydia antigen, for inducing an immune response against Chlamydia
PT psitacci, Chlamydia pneumoniae, other Chlamydia species, or a
PT non-chlamydia infection -
XX
PS Claim 6; Page 46-47; 100pp; English.
XX
CC The invention relates to a vaccine comprising a pharmaceutical carrier
CC and at least one polynucleotide having a Chlamydia sequence or at least
CC one Chlamydia antigen. The polynucleotide sequences are obtained
CC from cloned expression library of fragmented genomic DNA (expressed in
CC the vector pCMV-Ubi(+P3). Also included are immunising an animal
CC comprising providing to the animal at least one Chlamydia antigen or its
CC antigenic fragment (expressed from the cloned polynucleotides) to induce
CC an immune response (the proteins are chosen by transforming a vertebrate
CC animal with constituents of the library and choosing those which elicit
CC the best immune response, and then expressing those clones in cell

CC culture and purifying the protein), preparing antibodies against a
CC Chlamydia antigen (comprising identifying a Chlamydia antigen that
CC confers immune resistance against chlamydia bacterial infection when
CC challenged with the Chlamydia species in which the antigen was prepared,
CC generating an immune response in a vertebrate animal with the identified
CC antigen, and obtaining antibodies produced in the animal, the antibodies
CC are used to assay for the presence of chlamydia infection in a vertebrate
CC animal) and testing for antigens for a first disease state/infectious
CC agent (comprising determining an antigenic polypeptide or a nucleic acid
CC encoding an antigenic polypeptide from a second disease state or
CC infectious agent, obtaining a homologue of the antigenic polypeptide or
CC a nucleic acid encoding an antigenic polypeptide from a second disease
CC state or infectious agent for the first disease state/infectious
CC agent, and testing the homology to see if it is an antigenic
CC polypeptide or a nucleic acid encoding an antigenic polypeptide for the
CC first disease state or infectious agent). The vaccine, antigens and
CC polynucleotides are useful for inducing a protective immune response in
CC vertebrate animals against C. psitacci, C. pneumoniae, other species of
CC Chlamydia, or a non-chlamydia infection. The antigens are also useful for
CC antibody preparation techniques. Chlamydia species are responsible
CC for blindness, sexually transmitted disease, community-acquired
CC pneumonia and act as co-factors in atherosclerotic plaque formation in
CC coronary heart disease. C. psittaci in particular is a cause of mastitis,
CC infertility and abortion in cattle. The present sequence is one of the
CC cloned Chlamydia psittaci genomic DNA fragments of the invention.
XX
SQ Sequence 2520 BP; 774 A; 584 C; 490 G; 672 T; 0 other;

Alignment Scores:

Pred. No.:	1.29e-103	Length:	2520
Score:	1497.00	Matches:	357
Percent Similarity:	56.21%	Conservative:	132
Best Local Similarity:	41.03%	Mismatches:	321
Query Match:	34.85%	Indels:	60
DB:	25	Gaps:	25

US-09-830-446-27 (1-841) x ABX99183 (1-2520)



```
Qy        521 PheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTyr 540
              |||   |||:::|||:::   ||||||   :::::::::          ||||||   |||
Db       1564 TTCTCTGACCTCAGAGCTATACAAAACTTAATGGATATTAGCGTCAATGGCGCTGACTAC 1623

Qy        541 GluLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAsn 560
                 :::   |||||||||:::|||:::::|||   ||||||:::||||||   :::
Db       1624 CATAGAGGTTTTTGGGTATCCGGTCTAGCTAACTTCTTACACAAAAGTGGCTCTGATACT 1683

Qy        561 GlnArgLysPheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArgMetPro 580
              :::|||||||||||||||   |||   |||       :::|||          :::   |||
Db       1684 AAACGCAAGTTCCGTCACAATAGCGCCGGATACGCTTTAGGCGTCTACGCAAAAACTCCT 1743

Qy        581 GlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPhe 600
                  |||       |||       |||   |||||||||   :::||||||||||||
Db       1744 TCTGATGATATTTTCAGTGCGGCTTTCTGCCAACTCTTCGGAAAGGACAAAGACTATTTA 1803

Qy        601 MetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSer 620
              ::::::   |||   |||       ||||||||||||||||       ||||||       |||
Db       1804 GTGTCGAAAAACAACGCCAACATTTACGCAGGTTCTCTCTATTATCAGCAT---ATCTCC 1860

Qy        621 LeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuPro 640
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Db       1861 TATTGGAGC------------------------GCTTGGCAGAATCTGCTACAAAAC 1893

Qy        641 TyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAsp 660
              :::           |||                 ||||||:::|||   |||
Db       1894 ACTATCGGTGCAGAAGCTCCGTTAGTCCTTAACGCACAGTTAACTTATTGTCATGCTTCA 1953

Qy        661 HisArgMetLysThrGlu---------SerLeuProProProProProThrLeuSerThr 677
              :::   |||||||||             :::       |||           |||   :::
Db       1954 AACGACATGAAAACCAACATGACGACTACTTACGCTCCTCGTAAAACAACGTATGCAGAA 2013

Qy        678 AspHisThrSerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAlaVal 697
                        |||||           :::       |||||||||          |||   :::
Db       2014 ATCAAGGGTGATTGGGGTAACGATTGTTTCGGAGTCGAGCTTGGTGCAACTGTGCCTATC 2073

Qy        698 GluAsnThrSerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGlnAla 717
              :::       |||           |||       |||:::||||||:::|||   |||
Db       2074 CAAACAGAATCTTCTCTC---CTATTCGATATGTACTCACCTTTCCTGAAGTTTCAACTT 2130

Qy        718 ValTyrAlaArgGlnAspSerPheValGluLeuGlyAla---IleSerArgAspPheSer 736
              |||:::       ||||||   |||   |||       :::           |||   |||
Db       2131 GTGCATACGCACCAAGATGACTTTAAGGAAAACAATAGCGATCAGGGAAGATACTTCGAA 2190

Qy        737 AspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPheAla 756
                 |||:::|||   ||||||::::::|||:::|||||||||   |||   |||||||||
Db       2191 AGCAGCAATCTCACCAACCTTTCTCTGCCTATCGGCATCAAGTTTGAG---AGATTTGCT 2247

Qy        757 GluGln---------TyrTyrHisValValAlaMetTyrSerProAspValCysArgSer 773
                           |||||||||   |||   ||||||||||||:::   |||||||
Db       2248 AACAACGATACAGCTTCTTATCATGTCACTGCTGCTTATTCTCCTGATATCGTAAGAAGT 2307

Qy        774 AsnProLysCysThrThrThrLeuLeuSerAsnGlnGlySer------TrpLysThrLys 791
              ||||||   |||||||||:::||||||   :::       |||       |||   ||||||
Db       2308 AACCCTGACTGTACTACTTCTCTGTTAGTAAGCCCCGACTCTGCTGTCTGGGTAACGAAA 2367

Qy        792 GlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGly 811
                  :::||||||||||||   |||   ::::::||||||       :::   ||||||
Db       2368 GCCAACAACCTTGCGCGAAGCGCCTTCATGCTACAAGCAGGAAACTACTTGTCTTTAAGT 2427

Qy        812 AlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArgSerTyr 831
                  |||:::|||   ||||||||||||   ||||||||||||||||:::|||
Db       2428 CACAACATAGAAATCTTCAGCCAGTTCGGTTTCGAGCTCAGGGGATCTTCACGAACCTAT 2487

Qy        832 AsnValAspAlaGlySerLysIleLysPhe 841
              |||||||||   ||||||||||||:::|||
Db       2488 AACGTAGATCTCGGATCGAAGATCCAGTTC 2517

RESULT 12
ABL91241
ID   ABL91241 standard; DNA; 2787 BP.
XX
AC   ABL91241;
XX
DT   29-JUL-2002  (first entry)
XX
DE   Chlamydia pneumoniae cp6733 ORF DNA, SEQ ID NO:116.
XX
KW   Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KW   human respiratory disease; cardiovascular disease; atherosclerosis;
KW   coronary artery disease; carotid artery stenosis; myocardial infarction;
KW   cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW   strain CWL029; open reading frame; ORF; gene; ds.
XX
OS   Chlamydia pneumoniae.
XX
FH   Key             Location/Qualifiers
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FT   sig_peptide     1..51
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FT   mat_peptide     52..2784
FT                   /*tag=  c
FT                   /product= "Mature protein"
XX
PN   WO200202606-A2.
XX
PD   10-JAN-2002.
XX
PF   03-JUL-2001; 2001WO-IB01445.
XX
PR   03-JUL-2000; 2000GB-0016363.
PR   11-JUL-2000; 2000GB-0017047.
PR   21-JUL-2000; 2000GB-0017983.
PR   07-AUG-2000; 2000GB-0019368.
PR   18-AUG-2000; 2000GB-0020440.
PR   14-SEP-2000; 2000GB-0022583.
PR   10-NOV-2000; 2000GB-0027549.
PR   22-DEC-2000; 2000GB-0031706.
XX
PA   (CHIR-) CHIRON SPA.
XX
PI   Ratti G,  Grandi G;
XX
DR   WPI; 2002-154726/20.
DR   N-PSDB; ABB90583.
XX
PT   Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT   medicament for treatment or prevention of infection due to Chlamydia,
PT   preferably Chlamydia pneumoniae, and for diagnostic purposes  -
XX
PS   Claim 5; Page 97; 364pp; English.
XX
CC   Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
CC   pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
CC   them. The proteins are predicted to be immunogenic and may therefore be
CC   useful in vaccine production and for diagnostic purposes. Chlamydia
CC   pneumoniae is a common cause of respiratory disease in humans, and is
CC   also involved in the development of cardiovascular diseases such as
CC   atherosclerosis, coronary artery disease, carotid artery stenosis,
CC   myocardial infarction, cerebrovascular disease, aortic aneurysm,
CC   claudication and stroke. The proteins and nucleic acids of the invention
CC   may be used in vaccines and pharmaceutical compositions for the
CC   prevention or treatment of chlamydial infections, particularly Chlamydia
CC   pneumoniae infections. The proteins may also be used in the detection of
CC   Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
CC   DNA probe assay or blotting techniques for determining Chlamydia
CC   pneumoniae gene expression. The present sequence represents a
CC   specifically claimed DNA which encodes a Chlamydia pneumoniae protein of
CC   the invention.
XX
SQ   Sequence 2787 BP; 803 A; 644 C; 574 G; 766 T; 0 other;

Alignment Scores:
Pred. No.:              6.54e-99        Length:         2787
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Score:	1435.50	Matches:	340
Percent Similarity:	51.43%	Conservative:	147
Best Local Similarity:	35.90%	Mismatches:	335
Query Match:	33.42%	Indels:	125
DB:	24	Gaps:	15

US-09-830-446-27 (1-841) x ABL91241 (1-2787)

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Qy          1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
              ||||||      :::  ::::::|||:::|||  |||       |||      :::
Db          1 ATGAAGACTTCGATTCCTTGGGTTTTAGTTTCCTCCGTGTTAGCTTTCTCA---TGTCAC 57

Qy         21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
              |||       |||      |||   ||||||     :::||||||:::|||
Db         58 CTACAGTCACTAGCTAACGAGGAACTTTTATCACCTGATGATAGCTTTAATGGAAATATC 117

Qy         41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
                 :::   :::|||:::   |||||||||:::          |||   |||
Db        118 GATTCAGGAACGTTTACTCCAAAAACTTCAGCC-----------ACAACATATTCTCTA 165

Qy         61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCys 80
                    |||             |||  |||          |||   ||||||
Db        166 ACAGGAGATGTCTTCTTTTACGAG---CCTGGAAAAGGCACTCCCTTATCTGACAGTTGT 222

Qy         81 PheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr 100
              ||||||                :::|||   |||||||||   |||   |||   |||
Db        223 TTTAAGCAA------ACCACGGACAATCTTACCTTCTTGGGGAACGGTCATAGCTTAACG 276

Qy        101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsn 120
              |||       |||||||||   |||   :::|||||||||       |||       ||||||
Db        277 TTTGGCTTTATAGATGCTGGCACTCATGCAGGTGCTGCT---GCATCTACAACAGCAAAT 333

Qy        121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
              |||   :::|||   ||||||||||||   |||||||||       ||||||::::::|||
Db        334 AAGAATCTTACCTTCTCAGGGTTTTCCTTACTGAGTTTTGATTCCTCTCCTAGCACAACG 393

Qy        141 ValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAsp 160
              ||||||   |||   |||   ::::::       |||   :::::|||   :::
Db        394 GTTACTACAGGTCAGGGAACGCTTTCCTCAGCAGGAGGCGTAAATTTAGAAAATATTCGT 453

Qy        161 LysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180
              |||:::::::::       ||||||||||||   ||||||||||||||       |||
Db        454 AAACTTGTAGTTGCTGGGAATTTTTCTACTGCAGATGGTGGAGCTATCAAAGGAGCGTCT 513

Qy        180 ------------------------------------------------------------ 180

Db        514 TTCCTTTTAACTGGCACTTCTGGAGATGCTCTTTTTAGTAACAACTCTTCATCAACAAAG 573

Qy        180 ------------------------------------------------------------ 180

Db        574 GGAGGAGCAATTGCTACTACAGCAGGCGCTCGCATAGCAAATAACACAGGTTATGTTAGA 633

Qy        180 ------------------------------------------------------------ 180

Db        634 TTCCTATCTAACATAGCGTCTACGTCAGGAGGCGCTATCGATGATGAAGGCACGTCGATA 693

Qy        180 ------------------------------------------------------------ 180

Db        694 CTATCGAACAACAAATTTCTATATTTTGAAGGGAATGCAGCGAAAACTACTGGCGGTGCG 753

Qy        181 ----------------------------SerLeuLysIleAlaAsnAsnLysSerLeu 190
                                         |||   |||:::|||||||||:::|||
Db        754 ATCTGCAACACCAAGGCGAGTGGATCTCCTGAACTGATAATCTCTAACAATAAGACTCTG 813

Qy        191 SerPheIleGlyAsnSerSerSerThrArgGlyGlyAlaIleHisThrLysAsnLeuThr 210
                 |||       |||   :::   |||  ||||||||||||||   |||   |||
Db        814 ATCTTTGCTTCAAACGTAGCAGAAACAAGCGGTGGCGCCATCCATGCTAAAAAGCTAGCC 873

Qy        211 LeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGlyLys 230
              ||||||||||||||   |||   |||       |||         :::|||       |||
Db        874 CTTTCCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCATCAGCAACTCCTAAG 933

Qy        231 GlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGlyAsp 250
```

```
                ||||||||||||:::|||       ||||||   ||||||:::|||   ::::::|||:::
Db        934 GGGGGTGCTATCAGCATCGATGCCTCAGGAGAGCTCAGTCTTTCTGCAGAGACAGGAAAC 993

Qy        251 IleIlePheGluGlyAsnThrIle---------GlyAlaThrGlyThrValSerHisSer 267
              |||   |||       ||||||:::         |||:::|||   |||         :::
Db        994 ATTACCTTTGTAAGAAATACCCTTACAACAACCGGAAGTACCGATACTCCTAAACGTAAT 1053

Qy        268 AlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyHisThr 287
              ||||||:::::::|||::::::   |||   |||   |||||||||||||:::   ||||||
Db       1054 GCGATCAACATAGGAAGTAACGGGAAATTCACGGAATTACGGGCTGCTAAAAATCATACA 1113

Qy        288 IleTyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsn 307
              |||:::|||||||||||||||||||     |||::::::|||       |||   |||
Db       1114 ATTTTCTTCTATGATCCCATCACTTCAGAAGGAACCTCATCA------GACGTATTGAAG 1167

Qy        308 IleAsnSerProAspThrGlyAspAsnLysGluTyrThrGlyThrIleValPheSerGly 327
              ||||||:::           |||             |||   |||||||||:::|||||||||
Db       1168 ATAAATAACGGCTCTGCGGGAGCTCTCAATCCATATCAAGGAACGATTCTATTTTCTGGA 1227

Qy        328 GluLysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSerLysLeuGluGln 347
              |||   ||||||        |||   |||         |||       |||         |||
Db       1228 GAAACCCTAACAGCAGATGAACTTAAAGTTGCTGACAATTTAAAATCTTCATTCACGCAG 1287

Qy        348 AsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsn 367
                 |||:::         |||   ::::::|||:::       |||   |||   :::
Db       1288 CCAGTCTCCCTATCCGGAGGAAAGTTATTGCTACAAAAGGGAGTCACTTTAGAGAGCACG 1347

Qy        368 GlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeuValAla 387
              |||||||||:::|||   |||   |||   ||||||   |||||||:::|||
Db       1348 AGCTTCTCTCAAGAGGCCGGTTCTCTCCTCGGCATGGATTCAGGAACGACATTATCAACT 1407

Qy        388 AsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArgAsnGly 407
                    ||||||   :::|||||||||   ||||||:::|||||||||
Db       1408 ACAGCTGGGAGTATTACAATCACGAACCTAGGAATCAATGTTGACTCCTTAGGTCTTAAG 1467

Qy        408 LysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAspArgProVal 427
              :::   :::   |||:::|||       |||       :::   :::       :::
Db       1468 CAGCCCGTCAGCCTAACAGCAAAAGGTGCTTCAAATAAAGTGATCGTATCTGGGAAGCTC 1527

Qy        428 ValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeuAsnGluAspHisSer 447
              |||           :::   :::   |||::::::           :::   |||
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Qy        448 TyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIleSerAlaAspSerArg 467
              :::       :::|||::::::               |||:::       :::   |||
Db       1588 TTC---TCTCTATTAAAAATCACGGTTGATGCTGATGTTGATACTAACGTTGACATCAGC 1644

Qy        468 SerIleAspAlaVal--------------GlnSerProTyrGlyTyrGlnGlyLysTrp 482
              |||:::      |||                |||   ||||||:::||||||:::|||
Db       1645 AGCCTTATCCCTGTTCCTGCTGAGGATCCTAATTCAGAATACGGATTCCAAGGACAATGG 1704

Qy        483 ThrIleAsnTrpSerThrAsp-----------AspLysLysAlaThrValSerTrpAla 498
                 :::||||||:::||||||               |||:::||||||   :::|||
Db       1705 AATGTTAATTGGACTACGGATACAGCTACAAATACAAAAGAGGCCACGGCAACTTGGACC 1764

Qy        499 LysGlnSerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrp 518
              |||       |||   |||:::   |||:::::::::   ||||||   |||   ||||||
Db       1765 AAAACAGGATTTGTTCCCAGCCCCGAAAGAAAATCTGCGTTAGTATGCAATACCCTATGG 1824

Qy        519 GlySerPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAla 538
              |||   |||   |||:::||||||   |||       :::|||:::|||       |||
Db       1825 GGAGTCTTTACTGACATTCGCTCTCTGCAACAGCTTGTAGAGATCGGCGCAACTGGTATG 1884

Qy        539 ProTyrGluLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArg 558
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              ||||||::::::   |||||||||   |||||||||   |||:::|||   |||
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Qy        579 MetProGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAsp 598
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Db       2065 TGTTTTATCGCTCACAACAACTCTAGAACCTACGGTGGAACTTTATTCTTCAAGCACTCT 2124

Qy        619 AlaSerLeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeu 638

Db       2125 CATACCCTACAACCCCAAAACTATTTGAGATTAGGAAGAGCAAAGTTTTCTGAATCAGCT 2184

Qy        639 LeuProTyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHis 658

Db       2185 ATAGAAAAATTCCCTAGGGAAATTCCCCTAGCCTTGGATGTCCAAGTTTCGTTCAGCCAT 2244

Qy        659 ThrAspHisArgMetLysThrGlu------SerLeuProProProProProThrLeuSer 676

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Qy        677 ThrAspHisThrSerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAla 696

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Qy        697 ValGluAsnThrSerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGln 716

Db       2344 TTTGTTCTTTCCAACCCACATCCTCTTTTCAAGACCTTCATTCCACAGATGAAAGTCGAA 2403

Qy        717 AlaValTyrAlaArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSer 736

Db       2404 ATGGTTTATGTATCACAAAATAGCTTCTTCGAAAGCTCTAGTGATGGCCGTGGTTTTAGT 2463

Qy        737 AspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLys---LeuGluLysArgPhe 755

Db       2464 ATTGGAAGGCTGCTTAACCTCTCGATTCCTGTGGGTGCGAAATTCGTGCAGGGGGATATC 2523

Qy        756 AlaGluGlnTyr---TyrHisValValAlaMetTyrSerProAspValCysArgSerAsn 774

Db       2524 GGAGATTCCTACACCTATGATCTCTCAGGATTCTTTGTTTCCGATGTCTATCGTAACAAT 2583

Qy        775 ProLysCysThrThrThrLeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsn 794

Db       2584 CCCCAATCTACAGCGACTCTTGTGATGAGCCCAGACTCTTGGAAAATTCGCGGTGGCAAT 2643

Qy        795 LeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAla 814

Db       2644 CTTTCAAGACAGGCATTTTTACTGAGGGGTAGCAACAACTACGTCTACAACTCCAATTGT 2703

Qy        815 GluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArgSerTyrAsnValAsp 834

Db       2704 GAGCTCTTCGGACATTACGCTATGGAACTCCGTGGATCTTCAAGGAACTACAATGTAGAT 2763

Qy        835 AlaGlySerLysIleLysPhe 841

Db       2764 GTTGGTACCAAACTCCGATTC 2784
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```
RESULT 13
AAA30847
ID   AAA30847 standard; DNA; 2950 BP.
XX
AC   AAA30847;
XX
DT   29-AUG-2000  (first entry)
XX
DE   Chlamydia antigen CPN100634 full length coding sequence.
XX
KW   Chlamydia antigen; diagnosis; infection; community acquired pneumonia;
KW   therapy; upper respiratory tract disease; bronchitis; sinusitis;
KW   asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma;
KW   ds.
XX
OS   Chlamydia pneumoniae.
XX
FH   Key             Location/Qualifiers
FT   CDS             101..2887
FT                   /*tag=  a
FT                   /product= Chlamydia antigen CPN100634
XX
PN   WO200032794-A2.
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PD   08-JUN-2000.
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PF   01-DEC-1999;   99WO-CA01147.
XX
PR   01-DEC-1998;   98US-0110339.
PR   01-DEC-1998;   98US-0110340.
PR   01-DEC-1998;   98US-0110427.
PR   01-DEC-1998;   98US-0110428.
PR   01-DEC-1998;   98US-0110438.
XX
PA   (CONN-) CONNAUGHT LAB LTD.
XX
PI   Murdin AD,  Oomen RP,  Wang J;
XX
DR   WPI; 2000-412339/35.
DR   P-PSDB; AAY90236.
XX
PT   Nucleic acids encoding polypeptide antigens from Chlamydia useful for
PT   preventing, diagnosing and treating diseases such as community acquired
PT   pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
PT   asthma -
XX
PS   Claim 2; Fig 1; 174pp; English.
XX
CC   This sequence encodes a Chlamydia antigen of the invention, designated
CC   CPN100634. The nucleic acids (and their complementary sequences) may be
CC   used as diagnostic agents for detecting the presence of nucleic acids
CC   encoding Chlamydia antigens in samples according to standard methods,
CC   and therefore, for diagnosing Chlamydia infections. For example, they may
CC   be used as primers and probes for diagnostic polymerase chain reaction
CC   (PCR) assays. Antisense sequences may be used to down regulate
CC   expression of the proteins and may be used to treat infections. The
CC   nucleic acids may also be used to produce the protein antigens they
CC   encode according to standard recombinant DNA methodologies. The
CC   proteins may then be used as antigens for the production of antibodies
CC   (i.e. as vaccines) for preventing infection by Chlamydia. The
CC   antibodies may also be used as diagnostic reagents for detecting
CC   infections. Chlamydia is a pathogen implicated in the development of
CC   (for example) community acquired pneumonia, upper respiratory tract
CC   disease (especially bronchitis and sinusitis, asthmatic bronchitis,
CC   adult-onset asthma and acute exacerbations of asthma in adults.
XX
SQ   Sequence 2950 BP; 851 A; 670 C; 596 G; 833 T; 0 other;
```

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Alignment Scores:
Pred. No.:                7.02e-99        Length:          2950
Score:                    1435.50         Matches:         340
Percent Similarity:       51.43%          Conservative:    147
Best Local Similarity:    35.90%          Mismatches:      335
Query Match:              33.42%          Indels:          125
DB:                       21              Gaps:            15

US-09-830-446-27 (1-841) x AAA30847 (1-2950)

Qy          1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20

Db        101 ATGAAGACTTCGATTCCTTGGGTTTTAGTTTCCTCCGTGTTAGCTTTCTCA---TGTCAC 157

Qy         21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40

Db        158 CTACAGTCACTAGCTAACGAGGAACTTTTATCACCTGATGATAGCTTTAATGGAAATATC 217

Qy         41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60

Db        218 GATTCAGGAACGTTTACTCCAAAAACTTCAGCC-----------ACAACATATTCTCTA 265

Qy         61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCys 80
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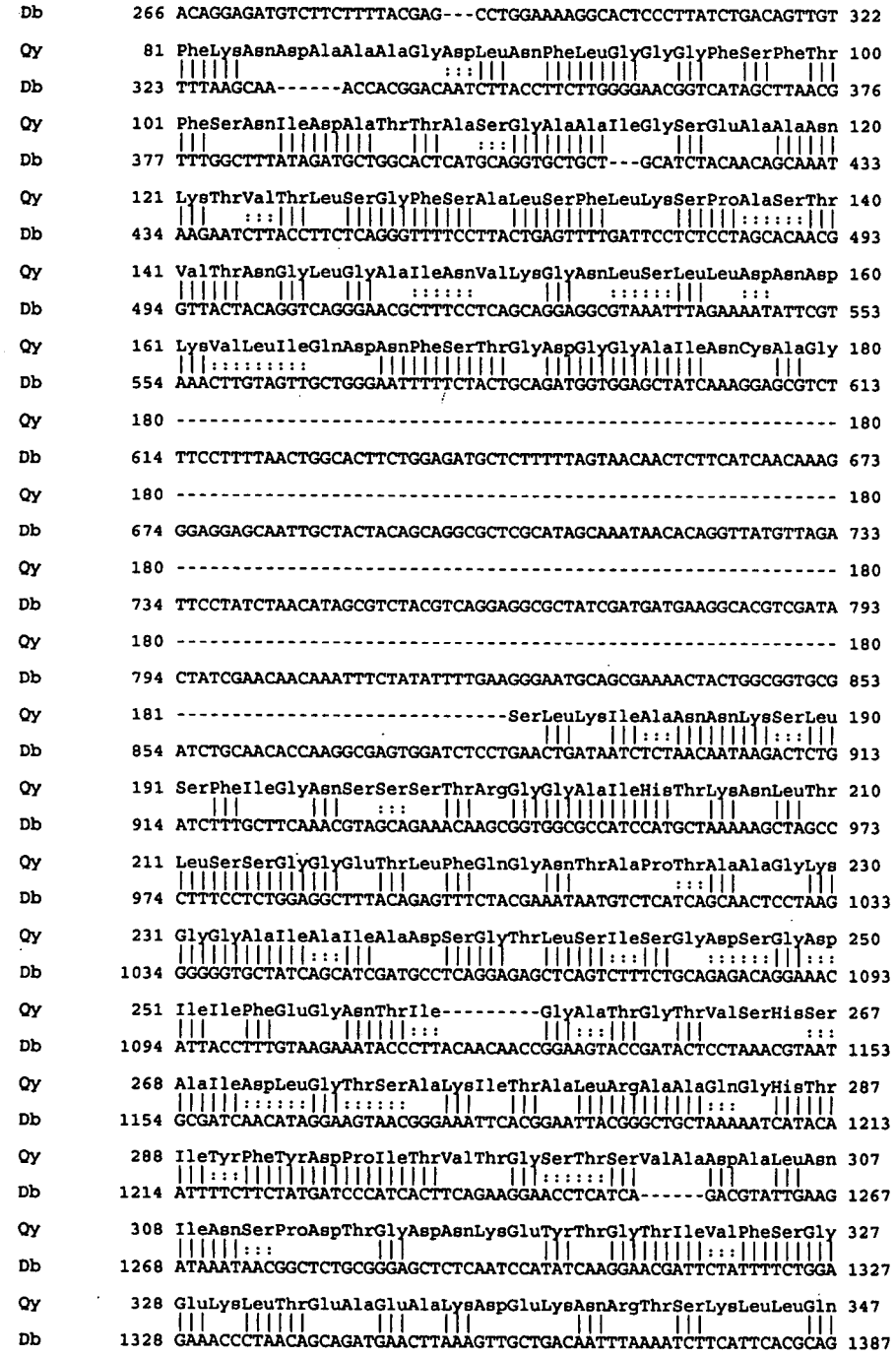
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Db 323 TTTAAGCAA------ACCACGGACAATCTTACCTTCTTGGGGAACGGTCATAGCTTAACG 376
Qy 101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsn 120
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Qy 141 ValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAsp 160
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Qy 161 LysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180
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Qy 180 -- 180
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Qy 180 -- 180
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Qy 180 -- 180
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Qy 180 -- 180
Db 794 CTATCGAACAACAAATTTCTATATTTTGAAGGGAATGCAGCGAAAACTACTGGCGGTGCG 853
Qy 181 ----------------------------SerLeuLysIleAlaAsnAsnLysSerLeu 190
Db 854 ATCTGCAACACCAAGGCGAGTGGATCTCCTGAACTGATAATCTCTAACAATAAGACTCTG 913
Qy 191 SerPheIleGlyAsnSerSerSerThrArgGlyGlyAlaIleHisThrLysAsnLeuThr 210
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Qy 211 LeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGlyLys 230
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Qy 231 GlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGlyAsp 250
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Db 2345 TCAGACAACCGTATGGAAACGCACTATACCTCATTGCCA---------- 2383
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Db 2384 GAATCCGAAGGTTCTTGGAGCAACGAGTGTATAGCTGGTGGTATCGGCCTAGACCTTCCT 2443

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Qy        717 AlaValTyrAlaArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSer 736
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Qy        835 AlaGlySerLysIleLysPhe 841
Db       2864 GTTGGTACCAAACTCCGATTC 2884
```

```
RESULT 14
AAX06816
ID   AAX06816 standard; DNA; 3200 BP.
XX
AC   AAX06816;
XX
DT   26-APR-1999  (first entry)
XX
DE   Chlamydia pneumoniae surface exposed protein Omp4 DNA.
XX
KW   Omp4; outer membrane protein 4; surface exposed protein; antigen;
KW   infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
XX
OS   Chlamydia pneumoniae.
XX
FH   Key             Location/Qualifiers
FT   CDS             205..2991
FT                   /*tag=  a
XX
PN   WO9858953-A2.
XX
PD   30-DEC-1998.
XX
PF   19-JUN-1998;   98WO-DK00266.
XX
PR   23-JUN-1997;   97DK-0000744.
XX
PA   (BIRK/) BIRKELUND S.
PA   (CHRI/) CHRISTIANSEN G.
XX
PI   Birkelund S,  Christiansen G,  Knudsen K,  Madsen A;
PI   Mygind P;
XX
DR   WPI; 1999-105610/09.
DR   P-PSDB; AAW88417.
XX
PT   Species-specific test for identifying mammals infected with
PT   Chlamydia pneumoniae - comprises detecting antibodies specific for
PT   outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT   these proteins
XX
PS   Claim 6; Page 35-40; 115pp; English.
XX
CC   This DNA sequence codes for the novel 98.9 kDa surface exposed
CC   protein Omp4 (see AAW88417) of the human respiratory pathogen
CC   Chlamydia pneumoniae.  By generating antibodies against C.
CC   pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
CC   was obtained which reacted with outer membrane proteins.  The
CC   antibody was used to identify the genes (see AAX06816-27) encoding
CC   Omp4-Omp15 proteins (see AAW88417-28) in an expression library of
CC   C. pneumoniae DNA.  The genes are situated in 2 gene clusters:
CC   Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
CC   the other, and encode polypeptides of about 89.6-100.3 kDa and
CC   about 56.1 kDa.  The invention provides a new species specific test
CC   for identifying mammals (including humans) infected with Chlamydia
CC   pneumoniae.  The test comprises detecting antibodies specific for
CC   Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC   membrane proteins, especially by PCR.  The proteins are also used
CC   in the diagnosis of C. pneumoniae infection in mammals.  The
CC   nucleic acids and proteins can also be used in the immunization of
CC   mammals, the nucleic acids being particularly useful as DNA
CC   vaccines for effecting in vivo expression of antigens.  The
CC   vaccines may also prevent atherosclerosis and bronchial asthma,
CC   which are possibly associated with C. pneumoniae.
XX
SQ   Sequence 3200 BP; 946 A; 708 C; 623 G; 923 T; 0 other;
```

Alignment Scores:			
Pred. No.:	7.78e-99	Length:	3200
Score:	1435.50	Matches:	340
Percent Similarity:	51.43%	Conservative:	147
Best Local Similarity:	35.90%	Mismatches:	335
Query Match:	33.42%	Indels:	125
DB:	20	Gaps:	15

US-09-830-446-27 (1-841) x AAX06816 (1-3200)

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Db        427 TTTAAGCAA------ACCACGGACAATCTTACCTTCTTGGGGAACGGTCATAGCTTAACG 480

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Qy        121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
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Qy        141 ValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAsp 160
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Qy        161 LysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180
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Qy        180 ------------------------------------------------------------ 180
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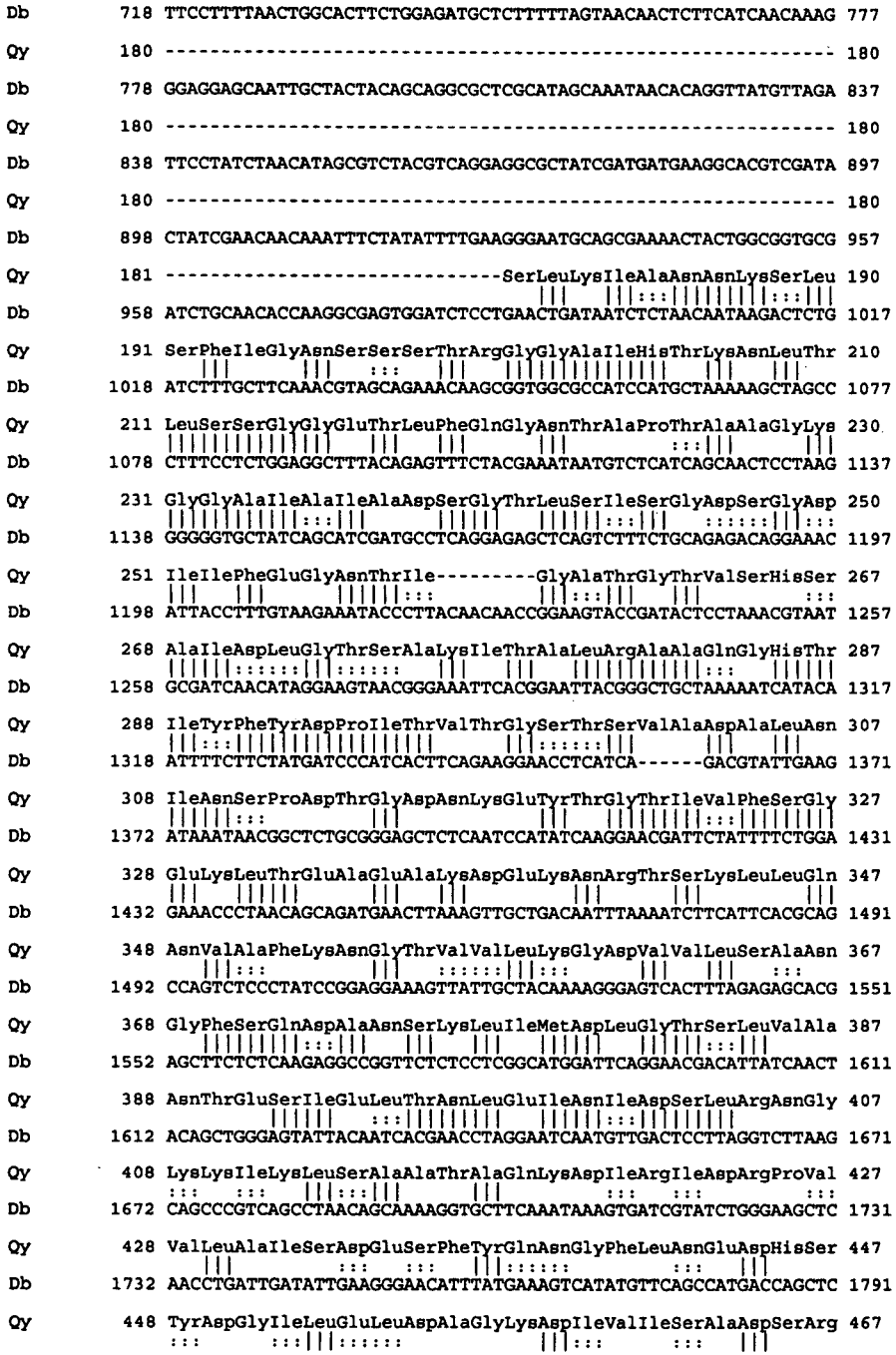
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Qy 180 ---------- 180
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Qy 180 ---------- 180
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Qy 181 ----------SerLeuLysIleAlaAsnAsnLysSerLeu 190
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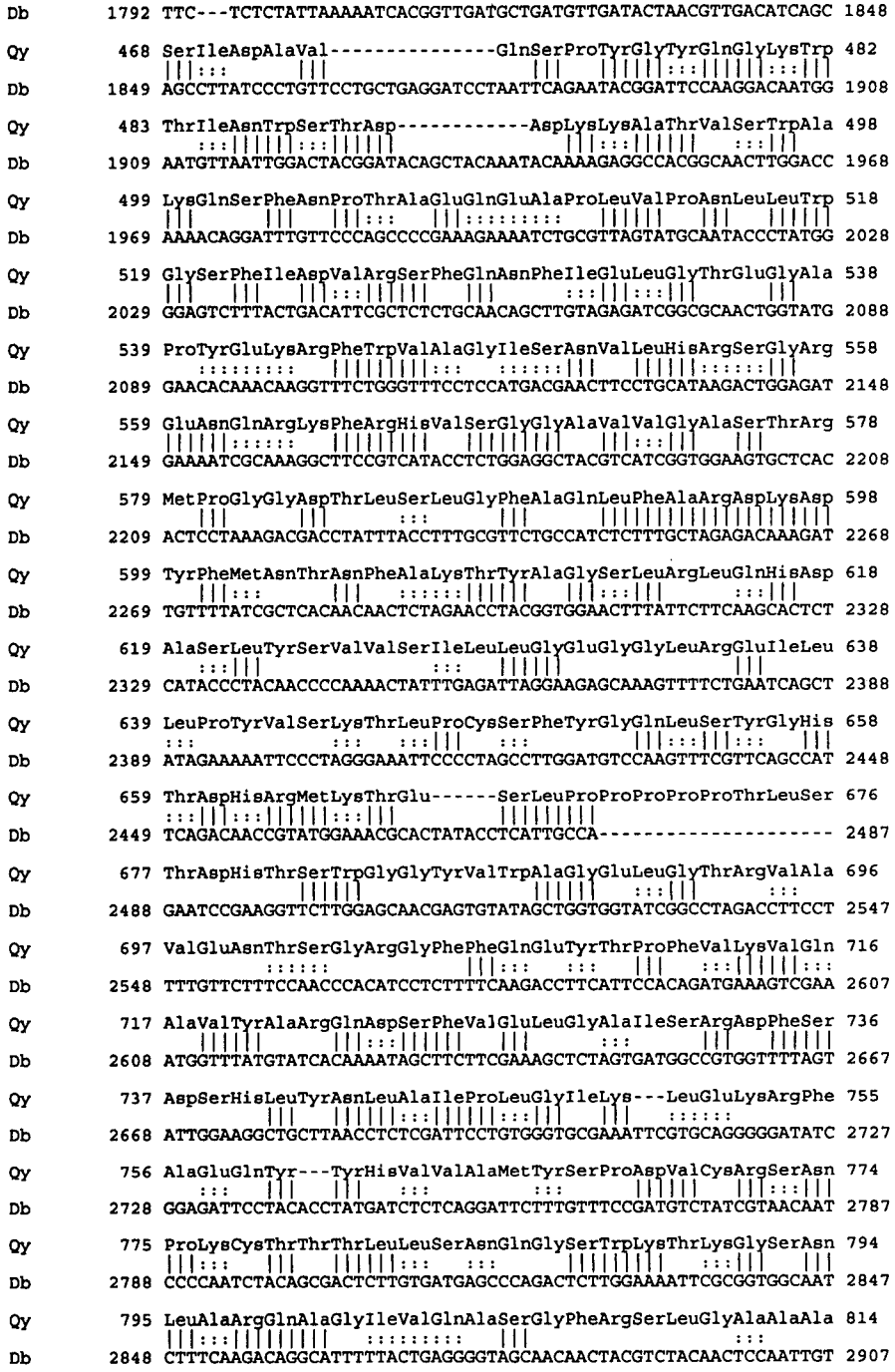
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Qy 483 ThrIleAsnTrpSerThrAsp----------AspLysLysAlaThrValSerTrpAla 498
Db 1909 AATGTTAATTGGACTACGGATACAGCTACAAATACAAAAGAGGCCACGGCAACTTGGACC 1968
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Qy 519 GlySerPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAla 538
Db 2029 GGAGTCTTTACTGACATTCGCTCTCTGCAACAGCTTGTAGAGATCGGCGCAACTGGTATG 2088
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Db 2149 GAAAATCGCAAAGGCTTCCGTCATACCTCTGGAGGCTACGTCATCGGTGGAAGTGCTCAC 2208
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Qy        835 AlaGlySerLysIleLysPhe 841
Db       2968 GTTGGTACCAAACTCCGATTC 2988

RESULT 15
AAC81914/c
ID   AAC81914 standard; DNA; 273254 BP.
XX
AC   AAC81914;
XX
DT   27-FEB-2001  (first entry)
XX
DE   Chlamydia pneumoniae genome DNA.
XX
KW   Genome; diagnosis; vaccine; ds.
XX
OS   Chlamydia pneumoniae.
XX
PN   WO200027994-A2.
XX
PD   18-MAY-2000.
XX
PF   12-NOV-1999;   99WO-US26923.
XX
PR   12-NOV-1998;   98US-0108279.
PR   08-APR-1999;   99US-0128606.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Stephens R,  Mitchell W,  Kalman S,  Davis R;
XX
DR   WPI; 2000-376516/32.
XX
PT   Isolated nucleic acid for use in diagnostic and analytical methods
PT   encodes genomic sequence of Chlamydia pneumoniae -
XX
PS   Claim 2; Page 128-320; 320pp; English.
XX
CC   This invention describes a novel nucleic acid (N1) encoding a Chlamydia
CC   pneumoniae protein (P1), given in the specification. The isolated nucleic
CC   acid is useful for diagnostic and analytical methods, such as,
CC   hybridization-based assays or amplification-based assays. The protein may
CC   be used for diagnostic purposes, for their enzymatic or structural
CC   activity, or as a vaccine. The invention also describes (1) a probe
CC   comprising a hybridizing fragment of N1; (2) an isolated nucleic acid
CC   (N2) that hybridizes under stringent conditions to N1; (3) an expression
CC   cassette comprising N1 under the transcriptional regulation of a
CC   transcriptional initiation region functional in an expression host, and a
CC   transcriptional termination region; (4) a cell comprising an expression
CC   cassette of (3) as part of an extrachromosomal element or integrated into
CC   the genome of a host cell as a result of induction of the expression
CC   cassette into the host cell, and the cellular progeny of the host cell;
CC   (5) a method for producing a P1 comprising growing a cell of (4) where
CC   the protein is expressed and isolating the protein free of other
CC   proteins; (6) a purified polypeptide composition comprising at least 50
CC   weight % of P1; and (7) a monoclonal antibody binding specifically to the
CC   peptide of (6).
XX
SQ   Sequence 273254 BP; 76423 A; 51054 C; 61965 G; 83812 T; 0 other;

Alignment Scores:
Pred. No.:                2.1e-96       Length:          273254
Score:                    1435.50       Matches:            340
Percent Similarity:       51.43%        Conservative:       147
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DB:                       21            Gaps:                15

US-09-830-446-27 (1-841) x AAC81914 (1-273254)

Qy          1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
Db      98031 ATGAAGACTTCGATTCCTTGGGTTTAGTTTCCTCCGTGTTAGCTTTCTCA---TGTCAC 97975

Qy         21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
Db      97974 CTACAGTCACTAGCTAACGAGGAACTTTTATCACCTGATGATAGCTTTAATGGAAATATC 97915

Qy         41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
Db      97914 GATTCAGGAACGTTTACTCCAAAAACTTCAGCC-----------ACAACATATTCTCTA 97867

Qy         61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCys 80
Db      97866 ACAGGAGATGTCTTCTTTTACGAG---CCTGGAAAAGGCACTCCCTTATCTGACAGTTGT 97810

Qy         81 PheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr 100
Db      97809 TTTAAGCAA------ACCACGGACAATCTTACCTTCTTGGGGAACGGTCATAGCTTAACG 97756

Qy        101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsn 120
Db      97755 TTTGGCTTTATAGATGCTGGCACTCATGCAGGTGCTGCT---GCATCTACAACAGCAAAT 97699

Qy        121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
Db      97698 AAGAATCTTACCTTCTCAGGGTTTTCCTTACTGAGTTTTGATTCCTCTCCTAGCACAACG 97639

Qy        141 ValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAsp 160
Db      97638 GTTACTACAGGTCAGGGAACGCTTTCCTCAGCAGGAGGCGTAAATTTAGAAAATATTCGT 97579

Qy        161 LysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180
Db      97578 AAACTTGTAGTTGCTGGGAATTTTTCTACTGCAGATGGTGGAGCTATCAAAGGAGCGTCT 97519

Qy        180 ------------------------------------------------------------ 180
Db      97518 TTCCTTTTAACTGGCACTTCTGGAGATGCTCTTTTTAGTAACAACTCTTCATCAACAAAG 97459

Qy        180 ------------------------------------------------------------ 180
Db      97458 GGAGGAGCAATTGCTACTACAGCAGGCGCTCGCATAGCAAATAACACAGGTTATGTTAGA 97399

Qy        180 ------------------------------------------------------------ 180
Db      97398 TTCCTATCTAACATAGCGTCTACGTCAGGAGGCGCTATCGATGATGAAGGCACGTCGATA 97339

Qy        180 ------------------------------------------------------------ 180
Db      97338 CTATCGAACAACAAATTTCTATATTTTGAAGGGAATGCAGCGAAAACTACTGGCGGTGCG 97279

Qy        181 ----------------------------SerLeuLysIleAlaAsnAsnLysSerLeu 190
Db      97278 ATCTGCAACACCAAGGCGAGTGGATCTCCTGAACTGATAATCTCTAACAATAAGACTCTG 97219

Qy        191 SerPheIleGlyAsnSerSerSerThrArgGlyGlyAlaIleHisThrLysAsnLeuThr 210
Db      97218 ATCTTTGCTTCAAACGTAGCAGAAACAAGCGGTGGCGCCATCCATGCTAAAAAGCTAGCC 97159

Qy        211 LeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGlyLys 230
Db      97158 CTTTCCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCATCAGCAACTCCTAAG 97099

Qy        231 GlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGlyAsp 250
Db      97098 GGGGGTGCTATCAGCATCGATGCCTCAGGAGAGCTCAGTCTTTCTGCAGAGACAGGAAAC 97039

Qy        251 IleIlePheGluGlyAsnThrIle---------GlyAlaThrGlyThrValSerHisSer 267
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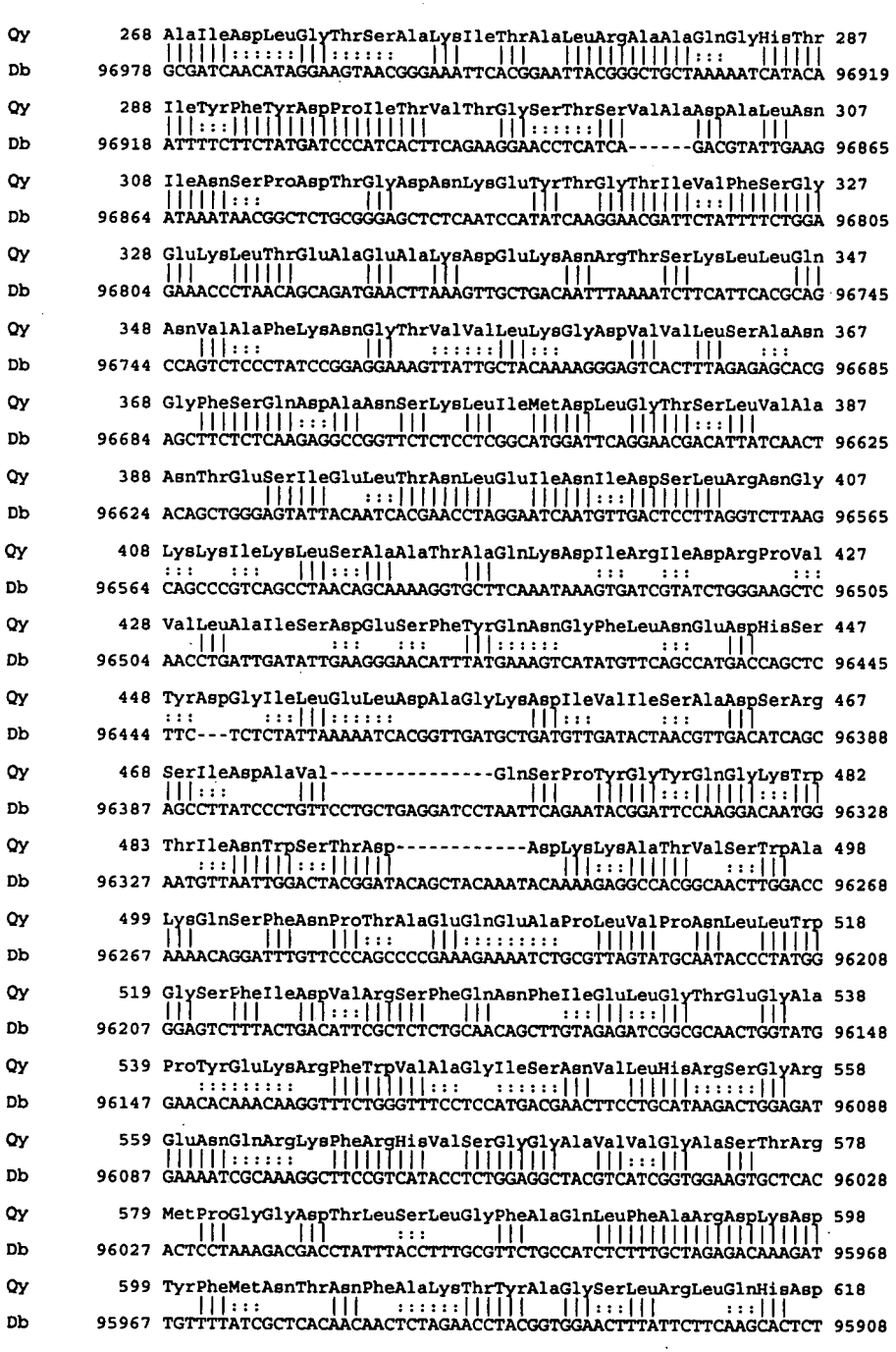

Search completed: January 29, 2004, 16:49:46
Job time : 1342 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 29, 2004, 10:21:11 ; Search time 4263 Seconds
(without alignments)
4794.761 Million cell updates/sec

Title: US-09-830-446-27
Perfect score: 4295
Sequence: 1 MKIPLRFLLISLVPTLSMSN.....FEWRGSSRSYNVDAGSKIKF 841

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09830446/runat_29012004_102102_19215/app_query.fasta_1.1031
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
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9: gb_est1:*
10: gb_est2:*
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12: gb_est3:*
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15: em_estfun:*
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17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	157	3.7	915	29	CNS06GB1	AL397475 T3 end of
c	2	155	3.6	624	12	BM276405	BM276405 PfESToaa8
c	3	155	3.6	979	29	CNS06PDW	AL409242 T7 end of
c	4	151	3.5	1094	29	CNS076CM	AL431228 T3 end of
	5	151	3.5	2293	11	AK032791	AK032791 Mus muscu
	6	150.5	3.5	1022	9	AL543791	AL543791 AL543791
c	7	150.5	3.5	1792	11	AY103948	AY103948 Zea mays
c	8	144	3.4	1164	13	BX405896	BX405896 BX405896
	9	142	3.3	977	29	CNS06T8C	AL414226 T7 end of
	10	142	3.3	1159	29	CNS0768D	AL431075 T7 end of
	11	141.5	3.3	1001	13	BQ963411	BQ963411 AGENCOURT
	12	140.5	3.3	634	10	BE583883	BE583883 8-11G-HA
	13	140	3.3	779	14	CA318878	CA318878 UI-M-FW0-
	14	137.5	3.2	788	12	BJ368874	BJ368874 BJ368874
c	15	135.5	3.2	698	14	CD284689	CD284689 G39178.95
	16	135	3.1	738	14	CA357513	CA357513 629879 NC
	17	135	3.1	933	14	CD459142	CD459142 Fg08_05d0
	18	135	3.1	1150	29	CNS079ZS	AL435950 T3 end of
c	19	134.5	3.1	719	14	CA855416	CA855416 PfESToac4
	20	133.5	3.1	849	28	AZ546009	AZ546009 ENTFW53TF
	21	133	3.1	755	14	CA486671	CA486671 WHE4334_E
	22	133	3.1	761	14	CA484808	CA484808 WHE4310_H
c	23	132.5	3.1	739	28	AY079536	AY079536 AY079536
c	24	132	3.1	882	13	BQ723746	BQ723746 AGENCOURT
	25	132	3.1	898	29	CNS04ALV	AL282028 Tetraodon
c	26	130.5	3.0	644	13	BQ838510	BQ838510 WHE2911_D
	27	130	3.0	731	14	CA485466	CA485466 WHE4319_B
	28	130	3.0	740	14	CA485375	CA485375 WHE4317_H
	29	130	3.0	833	12	BJ329437	BJ329437 BJ329437
	30	129.5	3.0	905	29	CNS06LF1	AL404099 T3 end of
c	31	129.5	3.0	965	29	CNS07DQ3	AL440785 T3 end of
	32	129	3.0	672	14	CD047378	CD047378 psHB027xJ
c	33	128.5	3.0	926	29	CNS06FRK	AL396774 T3 end of
	34	128.5	3.0	1200	14	CD497556	CD497556 CDA28-E08
	35	128	3.0	938	29	CNS07CG2	AL439128 T7 end of
c	36	127.5	3.0	804	13	BU602542	BU602542 AGENCOURT
	37	127.5	3.0	816	28	AZ535744	AZ535744 ENTCQ25TR
	38	127.5	3.0	863	14	CB588445	CB588445 AGENCOURT
c	39	127.5	3.0	2391	28	BH771003	BH771003 LLMGtag72
c	40	127	3.0	695	12	BJ388152	BJ388152 BJ388152
	41	127	3.0	807	12	BJ412244	BJ412244 BJ412244
	42	127	3.0	877	28	AZ531291	AZ531291 ENTBQ34TR
c	43	126.5	2.9	832	12	BM170146	BM170146 EST572669
c	44	126.5	2.9	1123	12	BM554825	BM554825 AGENCOURT
	45	126.5	2.9	2589	11	AK047537	AK047537 Mus muscu

ALIGNMENTS

RESULT 1
CNS06GB1
LOCUS CNS06GB1 915 bp DNA linear GSS 30-NOV-2001
DEFINITION T3 end of clone AS0AA003C01 of library AS0AA from strain CLIB 533 of Saccharomyces bayanus, genomic survey sequence.
ACCESSION AL397475
VERSION AL397475.1 GI:12150179
KEYWORDS GSS.
SOURCE Saccharomyces bayanus
ORGANISM Saccharomyces bayanus
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE 1 (bases 1 to 915)

```
  AUTHORS   Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
            Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
            de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
            Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
            Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
            Wincker,P. and Weissenbach,J.
  TITLE     Genomic exploration of the hemiascomycetous yeasts: 1. A set of
            yeast species for molecular evolution studies
  JOURNAL   FEBS Lett. 487 (1), 3-12 (2000)
  MEDLINE   20584711
   PUBMED   11152876
REFERENCE   2  (bases 1 to 915)
  AUTHORS   Bon,E., Neuveglise,C., Casaregola,S., Artiguenave,F., Wincker,P.,
            Aigle,M. and Durrens,P.
  TITLE     Genomic exploration of the hemiascomycetous yeasts: 5.
            Saccharomyces bayanus var. uvarum
  JOURNAL   FEBS Lett. 487 (1), 37-41 (2000)
  MEDLINE   20584715
   PUBMED   11152880
REFERENCE   3  (bases 1 to 915)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
            2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
            seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT     This GSS is part of a random genomic sequencing program of thirteen
            yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
            exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
            Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
            lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
            angusta, Debaryomyces hansenii var.  hansenii, Pichia sorbitophila,
            Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
            5 kb were prepared and both extremities were sequenced. See
            keywords for description of this sequence and for the sequence of
            the other extremity of this insert.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
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                     similarity to glucan 1,4-alpha-glucosidase and YAR066w ]
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                     similar to Saccharomyces cerevisiae ORF YOL155c [
                     similarity to glucan 1,4-alpha-glucosidase Sta1p and
                     YAR066w ]"
                     /evidence=not_experimental
BASE COUNT      158 a    256 c    199 g    299 t      3 others
ORIGIN

Alignment Scores:
Pred. No.:              1.4e-05       Length:         915
Score:                  157.00        Matches:        83
Percent Similarity:     38.64%        Conservative:   70
Best Local Similarity:  20.96%        Mismatches:     123
Query Match:            3.66%         Indels:         120
DB:                     29            Gaps:           15

US-09-830-446-27 (1-841) x CNS06GB1 (1-915)

Qy          9 LeuIleSerLeuValProThrLeuSerMetSerAsnLeuLeuGlyAlaAlaThrThrGlu 28
              :::::::::|||          ::::::      |||          :::|||:::
Db          4 GTTTTAGCCCTTTACTCTCAAAGTGCATTGGGCCAACTCTATAGCAATAGTACTTCACTT 63

Qy         29 GluLeuSerAlaSerAsnSerPheAspGlyThrThrSerThrThrSerPhe--------- 45
                    :::   |||::::::       :::||||||::::::||||||
Db         64 TCAAGCAACACCTCGTCGACCGTTGTTCCATCAACTTCGTCTAGTTCCTTTTCGATTAGT 123

Qy         46 SerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPheLysAspSerValVal 65
              |||:::   |||||||||   :::|||   ::::::   :::
Db        124 AGTACAATCACTTCGTCTGGTTCTGATGTCTCGAGCTCTATA---------------- 165

Qy         66 IleGluAsnValProLysThrGlyGluThrGlnSerThrSerCysPheLysAsnAspAla 85
                                |||||   |||   |||
Db        166 -----------------ACTGGGTCAACTTCGTCT---------------------- 183

Qy         86 AlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAsp 105
                                          |||   |||   |||         |||:::|||
Db        184 ----------------------GGTTCTGGCGCCTCA---------AGCTCTATAACT 210

Qy        106 AlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsnLysThrValThrLeu 125
                 :::|||:::||||||:::   :::   |||                 |||   :::
Db        211 GGGTCAACTTCGTCTGGTTCCGGTGTCTCGAGCTCTATTACTGGGTCAACCTCGTCTGGT 270

Qy        126 SerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeu 145
              ||||||   |||:::              |||       :::   ::::::|||
Db        271 TCCGGTGTCTCGAGC--------------TCTATTACTGGGTCAACTTCGTCTGGTTCT 315

Qy        146 GlyAla---IleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIle 164
              ||||||      ::::::   |||
Db        316 GGCGCCTCAAGCTCTATAACTGGG---------------------------------- 339

Qy        165 GlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGlySerLeuLysIle 184
                        ||||||      |||       ::::::   :::   |||
Db        340 -----------TCAACCTCGTCCGGTTCTGGTGTCTCGAGCTCAGCCTCT--------- 378

Qy        185 AlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArgGlyGlyAlaIle 204
                        |||   |||   :::   :::|||:::|||:::   |||       :::
Db        379 ---------CCATCTGGTTCCGGTGTCTCGAGTTCAGCCTCTTCATCTGGTTCCGGTGTC 429

Qy        205 HisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAla 224
              :::                       ||||||                  :::   :::
Db        430 TCCAGTTCAGCCTCTCCATCTGGTTCTGGT-----------GTCTCGAGTTCAGCCTCT 477

Qy        225 ProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIle 244
              |||:::   :::|||         :::   :::   :::   ||||||      |||
Db        478 CCATCTGGTTCTGGTGTCTCGAGTTCAGCCTCTCCATCTGGTTCTGGTGTCTCGAGCTCA 537

Qy        245 SerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAlaThrGlyThrVal 264
              :::      ||||||      :::           :::          :::|||:::
Db        538 GCCTCTCCATCTGGTTCAGGTGTCTCGAGTTCAGCCTCGCCATCCGGTTCTGGTTCTGGT 597

Qy        265 SerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGln 284
              |||   |||           |||   |||:::   ||||||
Db        598 TCTGGTTCAGGCTCCGGTTCCGGTGTTTCGAGCACTATCACT----------------- 639

Qy        285 GlyHisThrIleTyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAsp 304
                                          |||   |||||||||   :::   :::
Db        640 ----------------------CAATCTACTCCAACCGGATCCGGTGCCTCAAGTACT 675

Qy        305 AlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGluTyrThrGlyThrIleVal 324
                  :::   :::|||      ||||||
Db        676 ATCACTTCCTTCTCATCTTCTGGCACAGGA----------------------GCTACT 711

Qy        325 PheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSerLys 344
                 ||||||
Db        712 GCCTCTGGT------------------------------------------------- 720

Qy        345 LeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLys--------------- 359
                       :::::::::      :::||||||:::   |||
Db        721 ---------TCCCTTTCTTCTAACGATGGTACTATATACTTACCATCCACAACAATTTTC 771

Qy        360 GlyAspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMet 379
              ||||||:::   |||:::   :::   |||:::   ||||||         :::   :::
Db        772 GGCGATATCACACTTACCGGTGATGTATTTGCTACAGATGCA---------GTTGAAATC 822

Qy        380 AspLeuGlyThrSer------------LeuValAlaAsnThrGluSer 391
                 |||   :::            :::|||   ||||||:::|||
Db        823 GCCGCTGGSGCAAATTAACCCTTCTTGATGGTGACAAATACGGATTCT 870
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RESULT 2
BM276405/c
LOCUS       BM276405                624 bp    mRNA    linear   EST 20-DEC-2001
DEFINITION  PfESToaa82f11.y1 Plasmodium falciparum 3D7 gametocyte cDNA library
            Plasmodium falciparum 3D7 cDNA 5' similar to SW:CIGB_DICDI Q94481
            CIGB PROTEIN ;, mRNA sequence.
ACCESSION   BM276405
VERSION     BM276405.1  GI:17969762
KEYWORDS    EST.
SOURCE      Plasmodium falciparum 3D7
  ORGANISM  Plasmodium falciparum 3D7
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 624)
  AUTHORS   Tang,K., Cole,R., Chakrabarti,D., Haywood,R., Clifton,S., Pape,D.,
            Marra,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B.,
            Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Jentes,E., Ronko,I.,
            Tsagareishvili,R., Belaygorod,L., Franklin,C., Carr,L., Grow,A.,
            Maguire,L., Richey,J., Wadkins,J., Kennedy,S., Levinso,D.,
            Waterston,R., Wilson,R. and Sibley,D.
  TITLE     WashU Plasmodium EST Project
  JOURNAL   Unpublished
COMMENT     Contact: L. David Sibley
            WashU Plasmodium EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library was constructed by R. Haywood. DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: L. David Sibley
            (sibley@borcim.wustl.edu), Washington University
            Seq primer: -40UP from Gibco
            High quality sequence stop: 430.
FEATURES             Location/Qualifiers
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                     XhoI; The library was constructed by R Haywood. cDNAs were
                     synthesized  from ganetocyte poly(A)+ RNA by oligo d(T)
                     priming, size-selected  and directionally cloned into the
                     EcoRi (5' end) to XhoI (3' end)  sites of the Uni-ZAP XR
                     lambda vector (Stratagene). The primary  library was mass
                     excised as phagemid using the ExAssist helper  phage
                     (Stratagene). Clones were mass excised using the ExAssist
                     helper phage (Stratagene), the phagemids were precitptated
                     with  PEG 8000 and extracted with phenol/chloroform.
                     Phagemid DNA was  electroporated into DH10B cells. Clone
                     Availability: David Sibley,  Washington University."
BASE COUNT      261 a     61 c    158 g    144 t
ORIGIN

Alignment Scores:
Pred. No.:              1.27e-05        Length:         624
Score:                  155.00          Matches:        60
Percent Similarity:     45.65%          Conservative:   45
Best Local Similarity:  26.09%          Mismatches:     97
Query Match:            3.61%           Indels:         28
DB:                     12              Gaps:           8

US-09-830-446-27 (1-841) x BM276405 (1-624)

Qy          17 SerMetSerAsnLeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPhe 36
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Qy          37 AspGlyThrThrSerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThr 56
               |||   ||||||:::||||||   |||      |||||||||   :::
Db         563 TCAGGTATCACTTCTTCAACTAGTTCCTCAGGTATAACTTCTTCTACTAGT--------- 513

Qy          57 AsnTyrValPheLysAspSerValValIleGluAsnValProLysThrGlyGluThrGln 76
                           |||   :::     :::       :::|||   |||
Db         512 --------------TCTTCTGGTATAAGTTCTTCTACTACTTCTTCTGGTACAACCTCT 468

Qy          77 SerThrSerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGly 96
               ||||||:::         |||                        :::      |||
Db         467 TCAACTAAT---------AACTCAGGTATAACTTCTTCTACTAGTTCTTCTGGTATAAGT 417

Qy          97 PheSerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySer 116
               ||||||  :::   |||         ::::::|||:::|||                |||
Db         416 TTTTCTACCAGTTCTTCTGGTACCACCTCTTCAACTAGTTCCTCAGGTATAACTTCTTCT 357

Qy         117 GluAlaAlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSer 136
               :::::::::   |||   :::   :::       |||   ::::::
Db         356 ACTAGTTCTTCTGGTACAACCTCTTCAACTAGTTCTTCAGGTATAACT------------ 309

Qy         137 ProAlaSerThrValThrAsnGly---LeuGlyAlaIleAsnValLysGlyAsnLeuSer 155
               :::||||||   ::::::|||   :::   :::||||||       |||       |||
Db         308 ---TCTTCTACTAGTTCTTCTGGTATAATTTCTTCAATCAATTCTTCTGGTACAACTTCT 252

Qy         156 LeuLeuAspAsnAspLysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAla 175
               :::::::::   :::                |||||       |||
Db         251 TCAATCAATTCTTCTGGTATT-----------ACTTCTTCAACAACTTCTTCAGGTACC 204

Qy         176 IleAsnCysAlaGlySerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsn 195
               :::         |||       ||||||::::::   :::   |||   |||   :::
Db         203 ACTTCTTCAACTAATTCTTCAGATATCGCCTCTTCTACAACCTCTTCAGTTATTACTTCT 144

Qy         196 SerSerSerThrArgGlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGly--- 214
               |||   |||:::   |||           |||   :::|||       |||||||||
Db         143 TCAATTAGTTCTTCTGGT-----------ACAACCTCTTTAATTAATTCCTCAGGTATT 96

Qy         215 ---GlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAla 233
                        |||   |||   |||:::   :::|||       |||
Db          95 ACTTCTTCAATCAATTTTTCTGGTACAACTTCT---TCAGCAACTTCTTCAGGTATTACC 39

Qy         234 IleAlaIleAlaAspSerGlyThrLeuSer 243
               :::|||:::   ||||||      |||
Db          38 TCTTCAATTAGTTCTTCAGGTATAACTTCT 9

RESULT 3
CNS06PDW/c
LOCUS       CNS06PDW                979 bp    DNA     linear   GSS 05-JUL-2001
DEFINITION  T7 end of clone AV0AA013G05 of library AV0AA from strain CBS 379 of
            Saccharomyces exiguus, genomic survey sequence.
ACCESSION   AL409242
VERSION     AL409242.1  GI:12176588
KEYWORDS    GSS.
SOURCE      Saccharomyces exiguus
  ORGANISM  Saccharomyces exiguus
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (bases 1 to 979)
  AUTHORS   Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
            Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
            de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
            Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
            Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
            Wincker,P. and Weissenbach,J.
  TITLE     Genomic exploration of the hemiascomycetous yeasts: 1. A set of
            yeast species for molecular evolution studies
  JOURNAL   FEBS Lett. 487 (1), 3-12 (2000)
  MEDLINE   20584711
   PUBMED   11152876
REFERENCE   2  (bases 1 to 979)
  AUTHORS   Bon,E., Neuveglise,C., Lepingle,A., Wincker,P., Artiguenave,F.,
            Gaillardin,C. and Casaregola,S.
  TITLE     Genomic exploration of the hemiascomycetous yeasts: 6.
            Saccharomyces exiguus
  JOURNAL   FEBS Lett. 487 (1), 42-46 (2000)
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  MEDLINE   20584716
   PUBMED   11152881
REFERENCE   3  (bases 1 to 979)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
            2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
            seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT     This GSS is part of a random genomic sequencing program of thirteen
            yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
            exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
            Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
            lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
            angusta, Debaryomyces hansenii var.  hansenii, Pichia sorbitophila,
            Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
            5 kb were prepared and both extremities were sequenced. See
            keywords for description of this sequence and for the sequence of
            the other extremity of this insert.
FEATURES             Location/Qualifiers
     source          1. .979
                     /organism="Saccharomyces exiguus"
                     /mol_type="genomic DNA"
                     /strain="CBS 379"
                     /db_xref="taxon:34358"
                     /clone="AV0AA013G05"
                     /clone_lib="AV0AA"
                     /note="end : T7"
BASE COUNT      226 a    205 c    217 g    331 t
ORIGIN

Alignment Scores:
Pred. No.:              2.53e-05        Length:         979
Score:                  155.00          Matches:        83
Percent Similarity:     37.87%          Conservative:   45
Best Local Similarity:  24.56%          Mismatches:     138
Query Match:            3.61%           Indels:         72
DB:                     29              Gaps:           13

US-09-830-446-27 (1-841) x CNS06PDW (1-979)

Qy         26 ThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThrSerThrThrSerPhe 45
              ||||||::::::   ||||||      :::     ||||||   :::|||
Db        885 ACAACTGATGATAATAGTGCTCAAACTACCACTACAGGAACTGGTGCAACCGATGGTAAT 826

Qy         46 SerSerLysThrSerSer------------AlaThrAspGlyThrAsnTyrValPheLys 61
                 |||:::|||::::::            ||||||||||||
Db        825 GGTTCTCAAACTACAACTACAGGAACTGGTGCAACTGATGGTAATGGT------------ 778

Qy         62 AspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCysPhe 81
                                                  :::|||   :::|||
Db        777 --------------------------------TCTCAAACTACCACTACAGGAACCGGT 751

Qy         82 LysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThrPhe 101
                 |||                              |||  |||      |||
Db        750 GCAACTGAT-------------------------GGTAATGGTTCTCAAACTACAACC 718

Qy        102 SerAsnIleAspAla---------ThrThrAlaSerGlyAlaAlaIleGlySerGluAla 118
                       |||         ||||||   :::||||||      |||:::
Db        717 GATGGTAATAGTGCTCAAACTACCACTACAGGAACTGGTGCAACCGATGGTAAT------ 664

Qy        119 AlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAla 138
                          |||   :::|||       |||                :::   :::
Db        663 ---GGTTCTCAAACTACAACTACAGGAACTGGTGCAACTGAT------GGTAATGGTTCT 613

Qy        139 SerThrValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAsp 158
                 |||   |||   |||   ||||||   :::      |||:::|||:::      |||
Db        612 CAAACTACCACTACAGGAACCGGTGCAACCGATGGTAACGGCTCTTTAACTACAACTGAT 553

Qy        159 AsnAspLysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCys 178
                 ::::::                     :::|||       ||||||   :::
Db        552 GATAATAGTGCT------------CAAACTACCACTACAGGAACTGGTGCAACCGATGGT 505

Qy        179 AlaGlySerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSer 198
                    |||||||||                                      ::::::
Db        504 AACGGCTCTTTA----------------------------------------ACAACC 487

Qy        199 ThrArgGlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeu 218
                 |||   |||                  |||   :::|||::::::      :::
Db        486 ACTACAGGAACTGGTGCAACTGATGGTAACGGCTCTTTAACTACAACTGATGATAATAGT 427

Qy        219 PheGlnGlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAsp 238
                 |||      |||      |||   |||      |||
Db        426 GCTCAAATTACAACTACAGGAACTGGTGCAACTGATGGTAATGGTTCTCAAACTACAACC 367

Qy        239 SerGlyThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIle 258
                 |||      |||::::::      :::|||              :::|||||||
Db        366 GATGGTAATGGTTCTCTAACAACCACTACAGGAACTGGTGCAACCGATGGTAATGGTTCT 307

Qy        259 GlyAlaThr------GlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLys 276
                 :::|||      |||      |||   :::|||   |||   |||   ||||||:::
Db        306 CAAAGTACAACTGATGGTAATGGTTCTTTAACTGCAACTGAT---GGTAACAGTGCTCAA 250

Qy        277 IleThr---------------AlaLeuArgAlaAlaGlnGlyHisThrIleTyrPheTyr 291
                 |||                  :::|||   |||      |||::::::
Db        249 ACTACAACTGATGCAAATGGTTCTCTAACTGCAACCGATGGTAACAGTGCT--------- 199

Qy        292 AspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsnIleAsnSerPro 311
                       |||   ||||||:::   :::      ||||||   :::   |||
Db        198 ---CAAACTACCACTACAGGAACTGCTACAAATACCGATGCAACAGATGGTAACGGTTCC 142

Qy        312 AspThrGlyAspAsnLysGluTyrThrGlyThrIleValPheSerGlyGlu--------- 328
                 |||   |||:::         |||  |||          |||:::
Db        141 CAAACAACAGATGATGGTAATGGTACACATACGACAACTAATGGTGGTGATGGTAATGAG 82

Qy        329 ---------LysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSer 343
                             :::|||     :::|||:::         ||||||
Db         81 ATGGGATCATCATCAATGGATGCTATAGATAGGGACAAATCTACAGAAACAAGC 28

RESULT 4
CNS076CM/c
LOCUS       CNS076CM                1094 bp    DNA     linear   GSS 07-JUL-2001
DEFINITION  T3 end of clone BB0AA002F11 of library BB0AA from strain CBS 4732
            of Pichia angusta, genomic survey sequence.
ACCESSION   AL431228
VERSION     AL431228.1  GI:12214640
KEYWORDS    GSS.
SOURCE      Pichia angusta
  ORGANISM  Pichia angusta
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Pichia.
REFERENCE   1  (bases 1 to 1094)
  AUTHORS   Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
            Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
            de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
            Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
            Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
            Wincker,P. and Weissenbach,J.
  TITLE     Genomic exploration of the hemiascomycetous yeasts: 1. A set of
            yeast species for molecular evolution studies
  JOURNAL   FEBS Lett. 487 (1), 3-12 (2000)
  MEDLINE   20584711
   PUBMED   11152876
REFERENCE   2  (bases 1 to 1094)
  AUTHORS   Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F.
            and Dujon,B.
  TITLE     Genomic exploration of the hemiascomycetous yeasts: 13. Pichia
            angusta
  JOURNAL   FEBS Lett. 487 (1), 76-81 (2000)
  MEDLINE   20584723
   PUBMED   11152888
REFERENCE   3  (bases 1 to 1094)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
            2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
            seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
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COMMENT     This GSS is part of a random genomic sequencing program of thirteen
            yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
            exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
            Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
            lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
            angusta, Debaryomyces hansenii var.  hansenii, Pichia sorbitophila,
            Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
            5 kb were prepared and both extremities were sequenced. See
            keywords for description of this sequence and for the sequence of
            the other extremity of this insert.
FEATURES             Location/Qualifiers
     source          1. .1094
                     /organism="Pichia angusta"
                     /mol_type="genomic DNA"
                     /strain="CBS 4732"
                     /db_xref="taxon:4905"
                     /clone="BB0AA002F11"
                     /clone_lib="BB0AA"
                     /note="end : T3"
BASE COUNT      320 a    245 c    321 g    207 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:                7.88e-05       Length:          1094
Score:                    151.00         Matches:         79
Percent Similarity:       43.79%         Conservative:    55
Best Local Similarity:    25.82%         Mismatches:      131
Query Match:              3.52%          Indels:          42
DB:                       29             Gaps:            11

US-09-830-446-27 (1-841) x CNS076CM (1-1094)

Qy          9 LeuIleSerLeuValProThrLeuSerMetSerAsnLeuLeuGlyAlaAlaThrThrGlu 28
              |||:::|||   :::|||   ||||||  |||       :::       |||
Db        848 CTGCTATCTCCGATTCCGGAACTTTCAGC-TCTGCTACCTCAAGCTCAGGTTATACGTCA 790

Qy         29 GluLeuSerAlaSerAsnSerPheAspGlyThrThrSerThrThrSerPheSerSerLys 48
                 :::   |||          |||:::||||||:::   |||   ||||||
Db        789 AGCGCCGCCACCTCTGGATTTAGTTATGGGTCTACTTCAAGCGGCTCAGGTTCCAGCTCT 730

Qy         49 ThrSerSerAlaThrAspGlyThrAsnTyrValPheLysAspSerValValIleGluAsn 68
              :::|||||||||||||   |||::::::   :::|||      :::|||
Db        729 TCCAGCTCTGCCACTCCTGGATCAAGC---CTTTTCAGCTCTGCTGTC------------ 685

Qy         69 ValProLysThrGlyGluThrGlnSerThrSerCysPheLysAsnAspAlaAlaAlaGly 88
                    :::|||          :::||||||                |||::::::
Db        684 ---------TCCGGCTCCCGTGCCGCTACTTCT--------------GCCTCAAGTTAT 649

Qy         89 AspLeuAsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThr 108
              :::   |||              |||   |||                      |||
Db        648 GAGTCAAACACAGCTAGCTCTGGTTTAAGC-----------------TCTGCCGCTGCT 607

Qy        109 AlaSerGlyAlaAlaIleGlySerGluAlaAlaAsnLysThrValThrLeuSerGlyPhe 128
                 ||||||   :::      |||         ::::::|||         |||
Db        606 ATATCAGGTTTGAGCTCTGCTTCAAGTTATGGATCAAGGACTACTGTCTCTAGTTTAAGC 547

Qy        129 SerAlaLeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIle 148
              ||||||   :::          :::|||:::        ||||||   :::
Db        546 TCTGCCGCTGCTGGTTCCAGTTATGGCTCAAGCTCTACTGTCGCTGGTTTGAGCTCTGCC 487

Qy        149 AsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsnPhe 168
              :::     |||   ||||||        :::
Db        486 TCAAGTTACGGA---TTAAGCACCGCAGGCTCTGCCTCAAGTTATGGATCAAGCACCGCA 430

Qy        169 SerThrGlyAspGlyGlyAlaIleAsnCysAlaGlySerLeuLysIleAlaAsnAsnLys 188
              |||:::|||        |||        :::||||||        ::::::
Db        429 AGCTCTGGTTTGAGCTCTGCCGCTGCCATATCAGGCTCCAACTCTGCCTCAAGCTATGGC 370

Qy        189 SerLeuSerPheIleGlyAsnSerSerSerThrArgGlyGlyAlaIleHisThrLysAsn 208
              |||   :::   :::   :::   ||||||        ||:::   :::       :::
Db        369 TCAAGCACTGCTGTCTCTAGTTTAAGCTCTGCCGCTGCTGGTTCCAGTTATGGCTCAAGT 310

Qy        209 LeuThrLeuSerSer---------GlyGlyGluThrLeuPheGlnGlyAsnThrAlaPro 225
                    |||:::|||            |||      ::::::      |||:::::::::
Db        309 TCTACTATCTCTGGATCAAGCTATGGCTCAAGCTCTGTTGTCTCAGGCTCCAGCTCTGCC 250

Qy        226 ThrAla--------------AlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240
                 ::::::            ||||||  |||  :::  |||  :::
Db        249 TCAAGTTACGGATCAAGCACTGCAGGCTCTGGTTCAAGCTCTGCCTCAAGTTATGGCTCA 190

Qy        241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260
              :::   :::|||||||||   |||                    ::::::   |||:::
Db        189 AGCTCTACTATCTCAGGATCAAGC--------------TCTGCCTCAAGTTATGGCTCA 145

Qy        261 ThrGlyThrValSer------HisSerAlaIleAspLeuGlyThrSerAlaLysIleThr 278
              :::  |||||||||       ||||||      |||:::          :::
Db        144 AGCTCTACTGTCTCTGGTTTGACCTCTGCCTCAAGTTATGGCTCAGGCACCGCAGGCTCA 85

Qy        279 AlaLeuArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspPro---IleThrValThr 297
                 |||   :::|||                    |||   |||       ||||||
Db         84 GGTTTGAGCTCTGCTTCAAGT--------------TATGGACCAAGCTCTACTGTCGCT 40

Qy        298 GlySerThrSerValAla 303
                 |||   :::|||   |||
Db         39 GGTTTGAGCTCTGCTGCT 22

RESULT 5
AK032791
LOCUS       AK032791               2293 bp    mRNA    linear   HTC 05-DEC-2002
DEFINITION  Mus musculus 12 days embryo male wolffian duct includes surrounding
            region cDNA, RIKEN full-length enriched library, clone:6720452N09
            product:melanoma antigen, family D, 3-like, full insert sequence.
ACCESSION   AK032791
VERSION     AK032791.1  GI:26328570
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
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            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2293)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES            Location/Qualifiers
     source         1. .2293
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /strain="C57BL/6J"
                    /db_xref="FANTOM_DB:6720452N09"
                    /db_xref="taxon:10090"
                    /clone="6720452N09"
                    /sex="male"
                    /tissue_type="wolffian duct includes surrounding region"
                    /clone_lib="RIKEN full-length enriched mouse cDNA library"
                    /dev_stage="12 days embryo"
     CDS            <1. .2070
                    /note="unnamed protein product; melanoma antigen, family
                    D, 3-like (LocusLink|64836, GB|AB017108, evidence: BLASTN,
                    99%, match=640)
                    putative"
                    /codon_start=1
                    /protein_id="BAC28024.1"
                    /db_xref="GI:26328571"
                    /translation="GALSTSASFGGVLNGSAGFGGALNTNATFGGVLNGSAGFGGAMN
                    TNATFGGALNSNAGFGGAISTSTNFGGALNNSAGFGGAMNTSASFGGALNNSAGFGGA
                    ISTNATFGGALNNSAGFGGAISTNATFGGALNNSAGFGGAISTSASFGGTLNNSASFG
                    GAINTSASFGGVLNNSAGFGGAINTSANFGGALTNSAGFGGAISTSASFGGALNNSAG
                    FGGAISTSASFGGALNNSAGFGGAISTNASFGGAISNSPDFGGAFSTSVGFGGTLNTT
                    DFGSTHSNSISFGSAPTTSVSFGGSHSTNLCFGGAPSTSLCFGSASNTNLCFGGSNST
                    NCFSGATSANFNEGHSISFGNGLSTSAGFGNGLGTSAGFGSSLGTSTGFGGSLGPSAS
                    FNGGLGTSTGFGGGLGTSTDFSGGLNHNADFNGGLGNSAGFNGGLNTNTDFGGELGTS
                    AGFGDGLGSSTSFGAGLVTSDGFAGNLGTNTGFGGTLGTGAGFSVSLNNGNGFGNGPN
                    ASFNRGLNTIIGFGSGSNTSNGFTGEPNTGSSFSNGPSSIVGFSGGPSTGAGFCSGPS
                    TGGFGGGPSTGPGFGGPSTGPGFGGPSTGGGFGGPNTGGGFGGPSTGGGFGGPSTGGG
                    FGGPSTGGGFGGPSTAAGFGSGLSTSTGFGGGLNTSAGFSGGPPSTGTGFGGGASSHG
                    GCGFPYG"
     polyA_signal   2277. .2282
                    /note="putative"
     polyA_site     2293
                    /note="putative"
BASE COUNT      481 a    530 c    681 g    601 t
ORIGIN

Alignment Scores:
Pred. No.:                0.000245        Length:         2293
Score:                    151.00          Matches:        114
Percent Similarity:       36.31%          Conservative:   65
Best Local Similarity:    23.12%          Mismatches:     182
Query Match:              3.52%           Indels:         133
DB:                       11              Gaps:           25

US-09-830-446-27 (1-841) x AK032791 (1-2293)

Qy          8 LeuLeuIleSerLeuValProThrLeuSerMetSerAsnLeuLeuGlyAlaAlaThrThr 27
              :::|||          ||||||:::      |||      |||   ||||||   :::
Db        707 GTGCTGGCTTTGGCGGTGCCATCAGCACCAATGCCAGCTTTGGT-GGAGCAATCAGCAAC 765

Qy         28 Glu--------------GluLeuSerAlaSerAsnSerPheAspGlyThrThrSerThr 42
                                |||   |||       |||   ||||||   :::|||
Db        766 AGTCCTGACTTTGGTGGTGCATTCAGTACCAGTGTTGGCTTTGGTGGCACACTTAATACC 825

Qy         43 ThrSerPhe--------------------------------SerSerLysThrSerSer 51
              |||   |||                              |||:::   |||:::|||
Db        826 ACTGACTTTGGTAGTACCCATAGCAACAGCATTAGCTTTGGCAGTGCTCCCACTACCAGC 885

Qy         52 AlaThrAspGly------------ThrAsnTyrValPhe------------LysAspSer 63
                 :::   |||             ||||||      |||                 |||
Db        886 GTTAGCTTTGGTGGGTCTCATAGCACTAACCTCTGTTTCGGTGGAGCACCCAGCACCAGT 945

Qy         64 ValValIleGluAsnValProLysThr------------GlyGluThrGlnSerThrSer 79
              :::         :::          |||           |||   :::   ||||||:::
Db        946 CTCTGTTTTGGCAGTGCATCTAACACCAACCTATGCTTTGGAGGCTCTAACAGCACCAAC 1005

Qy         80 CysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPhe 99
              ||||||             :::|||          ||||||          |||   |||
Db       1006 TGCTTTAGTGGTGCTACCAGTGCC---------AATTTC---AATGAGGGGCACAGCATC 1053

Qy        100 ThrPheSerAsnIleAspAlaThrThrAlaSer---GlyAlaAlaIleGlySerGluAla 118
              :::|||   |||      :::|||:::|||      |||      :::|||:::   |||
Db       1054 AGTTTTGGGAATGGGCTAAGTACCAGTGCTGGATTTGGAAATGGGCTGGGCACCAGTGCT 1113

Qy        119 ------AlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSer 136
                    :::         |||   :::||||||
Db       1114 GGCTTTGGCAGCAGCCTTGGTACCAGCACTGGCTTTGGTGGA---------AGCTTAGGC 1164

Qy        137 ProAlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeu 156
              |||::::::::         ||||||||
Db       1165 CCCAGTGCTAGCTTCAATGGTGGCCTGGGCACC------------------------- 1197

Qy        157 LeuAspAsnAspLysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIle 176
                                              |||||||||   ||||||   :::
Db       1198 ----------------------------------AGCACTGGCTTTGGCGGTGGACTA 1221

Qy        177 AsnCysAlaGlySerLeuLysIleAlaAsnAsnLysSerLeuSerPhe---------Ile 193
                 :::                  |||   :::      |||          :::
Db       1222 GGCACCAGCACGGATTTCAGTGGTGGACTAAATCATAATGCTGACTTCAATGGAGGACTG 1281

Qy        194 GlyAsnSerSerSerThrArgGlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSer 213
              |||||||||:::        ||||||          |||
Db       1282 GGTAACAGTGCTGGCTTCAATGGTGGACTA------------AACACTAACACTGATTTT 1329
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Qy        214 GlyGlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAla 233
Db       1330 GGTGGTGAACTG---------GGCACTAGCGCTGGCTTTGGTGATGGACTGGGCAGCAGC 1380

Qy        234 IleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGlyAspIleIlePhe 253
Db       1381 ACCAGCTTTGGT---GCAGGACTGGTCACTAGTGATGGCTTTGCTGGTAACCTG------ 1431

Qy        254 GluGlyAsnThrIleGlyAlaThrGlyThrValSerHisSerAlaIleAspLeuGlyThr 273
Db       1432 ---GGCACCAATACTGGTTTTGGTGGCACA--------------------CTTGGCACT 1467

Qy        274 SerAlaLysIleThr---AlaLeuArgAlaAlaGlnGlyHisThrIleTyrPheTyrAsp 292
Db       1468 GGTGCAGGCTTTAGTGTAAGCCTCAACAATGGCAATGGCTTTGGC--------------- 1512

Qy        293 ProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsnIleAsnSerProAsp 312
Db       1513 ------------------------------------------------AATGGGCCTAAT 1524

Qy        313 ThrGlyAspAsnLysGluTyrThrGlyThrIleValPheSerGlyGluLysLeuThrGlu 332
Db       1525 GCCAGCTTCAACAGAGGACTGAATACCATCATTGGCTTTGGCAGTGGTTCCAACACCAGC 1584

Qy        333 AlaGluAlaLysAspGluLysAsnArgThrSerLysLeuLeuGlnAsnValAlaPheLys 352
Db       1585 AATGGCTTTACTGGTGAACCCAACACTGGCTCC-----------------AGCTTCAGT 1626

Qy        353 AsnGly-ThrValValLeuLysGlyAspValValLeuSerAlaAsnGlyPheSerGlnAs 372
Db       1627 AATGGACCCAGTTCTATTGTTGGCTTTAGTGGTGGACCAAGCACTGGTGCTGGCTTCTGC 1686

Qy        372 pAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeuValAlaAsnThrGluSerIl 392
Db       1687 AGTGGACCAAGCACTGGTG-----------GCTTCGGTGGTGGACCAAGTACAGGACCT 1734

Qy        392 eGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArgAsnGlyLysLysIleLysLe 412
Db       1735 G-----------------GCTTCGGTGGACCAAGTACAGGACCTGGCTTCGGTGGACCA 1776

Qy        412 uSerAlaAlaThrAlaGlnLysAspIleArgIle--------------AspArgProVa 427
Db       1777 AGCACTGGAGGTGGCTTTGGAGGACCAAATACTGGAGGTGGCTTTGGAGGACCAAGCACT 1836

Qy        427 lValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeuAsnGluAspHisSe 447
Db       1837 GGAGGTGGCTTTGGAGGACCAAGCACTG--------------------GAGGTGGCTTC 1875

Qy        447 rTyrAspGlyIleLeuGluLeuAspAlaGlyLysAsp 459
Db       1876 GGAGGACCAAGCACTGGAGGTG---GCTTCGGAGGAC 1909
```

RESULT 6
AL543791
LOCUS AL543791 1022 bp mRNA linear EST 31-MAY-2003
DEFINITION AL543791 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI005YD03 5-PRIME, mRNA sequence.
ACCESSION AL543791
VERSION AL543791.2 GI:31265637
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1022)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 15, 2001 this sequence version replaced gi:12876270.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10829.f For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI005CB02QP1&cluster=10829.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DI005CB02QP1.
FEATURES Location/Qualifiers
source 1. .1022
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI005YD03"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 195 a 282 c 277 g 265 t 3 others
ORIGIN

Alignment Scores:

Pred. No.:	8.02e-05	Length:	1022
Score:	150.50	Matches:	86
Percent Similarity:	40.43%	Conservative:	45
Best Local Similarity:	26.54%	Mismatches:	104
Query Match:	3.50%	Indels:	89
DB:	9	Gaps:	15

US-09-830-446-27 (1-841) x AL543791 (1-1022)

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Qy         17 SerMetSerAsnLeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPhe 36
Db        159 AGTTTTAGTGGCCCACTCAGCACCAGTGCCACTTTCAGTGGTGGAGCCAGCTCTGGCTTT 218

Qy         37 AspGlyThrThrSerThrThrSer---------------------------------- 44
Db        219 GGAGGCACACTCAGCACCACGGCTGGCTTTAGTGGTGTACTCAGCACTAGCACCAGCTTT 278

Qy         45 --------------------------PheSerSerLysThrSerSerAlaThrAspGly 55
Db        279 GGCAGTGCACCCACAACGAGCACAGTCTTCAGTAGTGCGCTTAGCACCAGCACT---GGC 335

Qy         56 ThrAsnTyrValPheLysAspSerValValIleGluAsnValProLysThr--------- 72
Db        336 TTTGGAGGCATACTCAGCACCAGTGTCTGTTTTGGTGGCTCTCCCAGCTCCAGTGGTAGC 395

Qy         73 ---GlyGluThrGlnSerThrSer---CysPheLysAsnAspAlaAlaAlaGlyAspLeu 90
Db        396 TTTGGTGGTACACTCAGTACCAGTATCTGCTTC---------------------------- 428

Qy         91 AsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThrAlaSer 110
Db        429 -----------GGTGGCTCTCCCTGCACCAGCACTGGCTTTGGAGGCACACTTAGCACC 476

Qy        111 GlyAlaAlaIleGly---------SerGluAlaAlaAsnLysThrValThrLeuSerGly 127
Db        477 AGTGTCTCCTTTGGTGGCTCTTCCAGCACCAGTGCCAATTTTGGTGGTACACTAAGT--- 533

Qy        128 PheSerAlaLeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAla 147
Db        534 ---ACCAGCATCTGCTTTGATGGCTCTCCCAGCACTGGTGCTGGCTTTGGT---GGTGCT 587

Qy        148 IleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsn 167
Db        588 CTCAACACCAGTGCCAGCTTTGGC--------------AGTGTGCTC---------AAC 623

Qy        168 PheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly-SerLeuLysIleAlaAsnAs 187
Db        624 ACCAGTACTGGTTTTGGTGGTGCTATGAGCACCAGTGCTGACTTTGGCGGTACACTAAGC 683
```

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Qy        187 nLysSerLeuSerPheIleGly-----------------------------------As 195
              |||:::   |||   |||                                       ||
Db        684 ACACAGTGTCTGCTTTGGTGGCTCTCCTGGCACCAGTGTCAGCTTTGGCAGTGCACTCAA 743

Qy        195 nSerSerSerThrArgGlyGlyAlaIleHisThrLys---------AsnLeuThrLeuSe 212
              |:::::::::     |||||||||:::   |||                 ||||||||
Db        744 CACCAATGCTGGTTATGGTGGTGCTGTCAGCACAAACACTGACTTTGGTGGTACACTAAG 803

Qy        212 rSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGlyLysGlyGl 232
              |:::         ::::::      |||   :::      |||:::||||||   |||||
Db        804 CACC---------AGCGTCTGTTTTGGTGGCTCTCCCAGCACCAGTGCTGGCTTTGGTGG 854

Qy        232 yAlaIle-----------------AlaIleAlaAspSerGlyThrLeuSerIleSerGl 246
              ||||:::                 |||   |||   :::   |||   |||||
Db        855 TGCACTCAACACCAATGCCAGCTTTGGCTGTGCCGTCAGCACCAGTGCCAGCTTCAGTGG 914

Qy        246 yAsp-SerGlyAspIleIlePheGluGlyAsnThrIleGlyAlaThrGlyThrValSerH 266
              |   |||     ::::::                 :::|||    |
Db        915 TGCTGTCAGCACAGTTGCTT-------------------------GCTTCAGTGGTGC 947

Qy        266 isSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyH 286
              ||   :::     |||     :::      :::      :::   |||:::   ||||
Db        948 ACCAATCACCAACCCTGGCTTTGGCGGTGCATTTAGCACCAGTGCTGGCTTCGGTGGGGC 1007

Qy        286 isThrIle 288
              ||   :::
Db       1008 ACTTAGTA 1015

RESULT 7
AY103948/c
LOCUS       AY103948               1792 bp    mRNA    linear   HTC 16-OCT-2002
DEFINITION  Zea mays PCO124731 mRNA sequence.
ACCESSION   AY103948
VERSION     AY103948.1  GI:21207026
KEYWORDS    HTC.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 1792)
  AUTHORS   Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
            Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
  TITLE     Maize Mapping Project/DuPont Consensus Sequences for Design of
            Overgo Probes
  JOURNAL   Unpublished (2002)
REFERENCE   2  (bases 1 to 1792)
  AUTHORS   Coe,E.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2002) Maize Mapping Project, University of
            Missouri, Columbia, MO 65211, USA
COMMENT     If you are interested in getting corresponding physical clones,
            these are publicly available from ZmDB and may be found by BLAST
            searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
            www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
            maize cDNA sequences is either Virginia Walbot, Stanford or Pat
            Schnable, Iowa State, then clones may be requested from ZmDB:
            www.zmdb.iastate.edu.
FEATURES             Location/Qualifiers
     source          1. .1792
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /db_xref="MaizeDB:637267"
                     /db_xref="taxon:4577"
                     /clone_lib="Maize Mapping Project/DuPont Cornsensus
                     Library"
                     /note="this sequence is part of a project of EST
                     assemblies resulting from the application of public
                     contigs to seed DuPont contigs; this resource was
                     assembled by DuPont as part of a collaboration for the
                     overgo addressing of BACs in conjunction with the Maize
                     Mapping Project"

BASE COUNT      467 a    506 c    482 g    337 t
ORIGIN

Alignment Scores:
Pred. No.:                0.00019        Length:          1792
Score:                    150.50         Matches:         90
Percent Similarity:       35.75%         Conservative:    48
Best Local Similarity:    23.32%         Mismatches:      157
Query Match:              3.50%          Indels:          91
DB:                       11             Gaps:            14

US-09-830-446-27 (1-841) x AY103948 (1-1792)

Qy          7 PheLeuLeuIleSerLeuValProThrLeuSerMetSerAsnLeuLeuGlyAlaAlaThr 26
              :::||||||   ||||||   |||                         |||   ||||||
Db       1414 TGGCTGCTCTCCTCGCTTCCGCCT--------------------TTGTCGGCAGCGGTG 1376

Qy         27 ThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThrSerThrThrSerPheSer 46
                    :::||||||   |||       |||       |||       :::   |||
Db       1375 TTCTCTAGTGGAGCGGCGTCTGGCTCGGCTCCAGGCGCGGCATCAGTGGCGGCAGCATCT 1316

Qy         47 SerLysThrSerSerAlaThrAspGlyThrAsnTyrValPheLysAspSerValValIle 66
              :::
Db       1315 GCCTTG------------------------------------------------------ 1310

Qy         67 GluAsnValProLysThrGlyGluThrGlnSerThrSerCysPheLysAsnAspAlaAla 86
                ||||||      |||                                     ||||||
Db       1309 ------GTCCCGGGTGCTGGATCAGCG-------------------------GCGGCA 1283

Qy         87 AlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAla 106
              |||  ||||||          |||      :::          |||      |||
Db       1282 GCATCTGATTTGATTTCAGGTGCTGGATCAGCGGCAGCAGCAGGCTCGGCATCTGATTTG 1223

Qy        107 ThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsnLysThrValThrLeuSer 126
                 :::  :::||||||||      |||  |||   :::   |||      :::|||
Db       1222 GTTTCAGGCGCTGGAGCAGCAACAGCATCAGCAGCAGATTCAGCAACTGGTTTGGTCTCG 1163

Qy        127 GlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGly 146
              |||      |||   :::              ||||||   :::   :::|||   |||
Db       1162 GGCACTGGAGCAGCAGCA---------GGCTCGGCATCTGATTTGGTTTCAGGCGCCGGA 1112

Qy        147 AlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAsp 166
              |||                  |||      |||:::          |||:::
Db       1111 GCA------------GCAACAGCATCAGCAGCAGATTCAGCAACTAGTTTGGTCTCGGGC 1064

Qy        167 AsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGlySerLeuLysIleAlaAsn 186
                   :::      |||  |||  :::                    |||
Db       1063 ACTGGAGCAGCAGCAGCAGGTTCAGCAACTGATTTGGTGTCAGGCGCTGGAGCAGCAGCA 1004

Qy        187 AsnLysSerLeuSerPheIle---GlyAsnSerSerSerThrArgGlyGlyAlaIleHis 205
                   :::      :::   |||      ::::::         |||:::
Db       1003 GGCTCAGCAACTGATTTGGTGTCAGGCACTGGAGCAGCAGCAGCAGGCTCG------ 950

Qy        206 ThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaPro 225
                        :::||||||          ||||||   |||      |||
Db       949 -----------------GCATCTGGT---------TTGTTTTCAGGCGCTGGGGCAGGA 917

Qy        226 ThrAlaAlaGly--------------------LysGlyGlyAlaIleAlaIleAlaAsp 238
              ||||||||||||                  ||||||      |||
Db       916 ACAGCAGCAGGCTTGGCATCTGGTTTGGTTTCAGGCGCTGGGGCGAGAACAGCAGCAGGC 857

Qy        239 SerGlyThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIle 258
              |||   |||   |||:::||||||                        |||
Db       856 TCGGCAACTGATTCGGTCTCAGGCACTGGGGCA--------------GGAACAGCAGCA 812

Qy        259 GlyAlaThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThr 278
              |||:::   |||     :::      ::::::   |||   |||   |||      |||
Db       811 GGCTCGGCAGGAGCAGGGGCTGAGTTCTCAGTTGGGTTGCTTACTGGAGCTGGAGCCACA 752

Qy        279 AlaLeuArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGly 298
              |||         :::   |||           |||:::                  |||
Db       751 GCT---TCAGGCTCATCTGGCTTGGCATCTTCTTTCTTCTCCTCCGATTGCGCAAGAGGA 695
```

```
Qy        299 SerThrSerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGlu 318
              :::|||:::   :::         :::::::::
Db        694 GCTACAACAGCTTCAGCTGGTTTCTCAGTTTCT-------------------------- 662

Qy        319 TyrThrGlyThrIleValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGlu 338
              ::::::   :::   :::   :::|||      ::::::   |||
Db        661 TTCTCATCTTCTTCCATTGGCGCCGGAGCAGGAGTATCGTCCGCC-------------- 617

Qy        339 LysAsnArgThrSerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeu 358
                                     :::   ||||||         :::|||   :::
Db        616 ------------------------TTGTCTGCAGCCTTCTCAGCGTCATCAGTTTCAGTA 581

Qy        359 LysGlyAspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIle 378
                |||             |||:::   ||||||         :::   |||   :::
Db        580 ---GGAGCTTCCTTCGCCTCTTCAGCAGGCTTCATCTCCACGTCAGTCTCCTTTGTGCCA 524

Qy        379 MetAspLeuGlyThrSer 384
                  ||||||   |||
Db        523 TCTTCACTTGGGGCGTCC 506

RESULT 8
BX405896/c
LOCUS       BX405896               1164 bp    mRNA    linear   EST 13-MAY-2003
DEFINITION  BX405896 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
            CS0DM009YE14 5-PRIME, mRNA sequence.
ACCESSION   BX405896
VERSION     BX405896.1  GI:30635433
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1164)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 10458.r, and
            it belongs to a clone representative of this cluster. For more
            information about this cluster and the virtual cDNA, see
            http://www.genoscope.cns.fr/ Contact : Feng Liang Email :
            fliang@lifetech.com URL : http://fulllength.invitrogen.com/
            InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID :
            CS0AM009BC07QP1.
FEATURES             Location/Qualifiers
     source          1. .1164
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DM009YE14"
                     /tissue_type="FETAL LIVER"
                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL LIVER"
                     /note="Organ: liver; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
BASE COUNT      297 a    277 c    307 g    237 t     46 others
ORIGIN

Alignment Scores:
Pred. No.:                0.000472        Length:          1164
Score:                    144.00          Matches:         79
Percent Similarity:       40.21%          Conservative:    38
Best Local Similarity:    27.15%          Mismatches:      94
Query Match:              3.35%           Indels:          80
DB:                       13              Gaps:            15
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```
US-09-830-446-27 (1-841) x BX405896 (1-1164)

Qy         13 ValProThrLeuSerMetSerAsnLeuLeu-----------------GlyAlaAlaThr 26
              ||||||   |||   :::   :::   |||                       :::
Db        835 GTGCCAGCTTTAGTGGTGGAGTCAGCTCTAGTTTAGTGGCCCACTCAGCACCCAGTKGC 776

Qy         27 ThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThrSerThrThrSer------ 44
              |||           ||||||:::   |||   ||||||   |||||||||:::
Db        775 ACTTTCAGTGGTGGAGCCAGCTCTGGCTTTGGAGGCACACTCAGCACCACGGCTGGCTTT 716

Qy         45 ----------------------------------------------------------Phe 45
                                                                        |||
Db        715 AGTGGTGTACTCAGAACTAGCACCAGATTTGGCAGTGCACCCACAACGAGAACAGTCTTC 656

Qy         46 SerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPheLysAspSerValVal 65
              ||||||      |||:::   |||   |||         :::         ||||||
Db        655 AGTAGTGCGCTTAGCACCAGAACT---GGCTTTGGAGGCATACTCAGCACCAGTGTCTGT 599

Qy         66 IleGluAsnValProLysThr-----------GlyGluThrGlnSerThrSer---Cys 80
                       |||   :::             |||   |||   |||||||||   |||
Db        598 TTTGGTGGCTCTCCCAGCTCCAGTGGTAGCTTTGGTGGTACACTCAGTACCAGTATCTGC 539

Qy         81 PheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr 100
              |||                                       ||||||         |||
Db        538 TTC-----------------------------------GGTGGCTCTCCCTGCACC 518

Qy        101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGly---------SerGlu 117
                 :::             |||   ::::::      :::   |||         |||
Db        517 AGNACTGGCTTTGGAGGCACACTTAGCACCAGTGTCTCCTTTGGTGGCTCTTCCAGCACC 458

Qy        118 AlaAlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerPro 137
              :::||||||         |||||||||      :::::::::   |||      ||||||
Db        457 AGTGCCAATTTTGGTGGTACACTAAGT------ACCAGCATCTGCTTTGATGGCTCTCCC 404

Qy        138 AlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeu 157
                 :::          |||   ||||||:::|||         :::
Db        403 AGAACTGGTGCTGGCTTTGGT---GGTGCTCTCAACACCAGTGCCAGCTTTGGC------ 353

Qy        158 AspAsnAspLysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsn 177
                       ||||||         |||   |||||||||   |||||||||::::::
Db        352 ---------AGTGTGCTC---------AACACCAGTACTGGTTTTGGTGGTGCTATGAGC 311

Qy        178 CysAlaGlySerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGly--------- 194
              :::                      :::   |||:::   |||   |||
Db        310 ACCAGTGCTGACTTTGGCGGTACACTAAGCACCAGTGTCTGCTTTGGTGGCTCTCCTGGC 251

Qy        195 --------------------------AsnSerSerSerThrArgGlyGlyAlaIleHis 205
                                        |||:::::::::   |||||||||:::
Db        250 ACCAGTGTCAGCTTTGGCAGTGCACTCAACACCAATGCTGGTTATGGTGGTGCTGTCAGC 191

Qy        206 ThrLys---------AsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsn 222
              |||                  |||||||||:::         ::::::      |||
Db        190 ACCAACACTGACTTTGGTGGTACACTAAGCACC---------AGCGTCTGTTTTGGTGGC 140

Qy        223 ThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGlyThrLeu 242
              :::      |||:::||||||  |||||||||:::                |||
Db        139 TCTCCCAGCACCAGTGCTGGCTTTGGTGGTGCACTCAACACCAATGCCAGCTTTGGCTGT 80

Qy        243 SerIleSer------GlyAspSerGlyAspIle 251
              ::::::|||      |||:::||||||   :::
Db         79 GCCGTCAGCAATCCCGGGAATTCCGGACCGGTA 47

RESULT 9
CNS06T8C
LOCUS       CNS06T8C               977 bp    DNA     linear   GSS 05-JUL-2001
DEFINITION  T7 end of clone AW0AA029F08 of library AW0AA from strain CLIB 89 of
            Yarrowia lipolytica, genomic survey sequence.
ACCESSION   AL414226
VERSION     AL414226.1  GI:12187157
KEYWORDS    GSS.
SOURCE      Yarrowia lipolytica
  ORGANISM  Yarrowia lipolytica
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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            Saccharomycetales; Dipodascaceae; Yarrowia.
REFERENCE   1  (bases 1 to 977)
  AUTHORS   Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
            Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
            de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
            Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
            Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
            Wincker,P. and Weissenbach,J.
  TITLE     Genomic exploration of the hemiascomycetous yeasts: 1. A set of
            yeast species for molecular evolution studies
  JOURNAL   FEBS Lett. 487 (1), 3-12 (2000)
  MEDLINE   20584711
   PUBMED   11152876
REFERENCE   2  (bases 1 to 977)
  AUTHORS   Casaregola,S., Neuveglise,C., Lepingle,A., Bon,E., Feynerol,C.,
            Artiguenave,F., Wincker,P. and Gaillardin,C.
  TITLE     Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia
            lipolytica
  JOURNAL   FEBS Lett. 487 (1), 95-100 (2000)
  MEDLINE   20584727
   PUBMED   11152892
REFERENCE   3  (bases 1 to 977)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
            2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
            seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT     This GSS is part of a random genomic sequencing program of thirteen
            yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
            exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
            Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
            lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
            angusta, Debaryomyces hansenii var.  hansenii, Pichia sorbitophila,
            Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
            5 kb were prepared and both extremities were sequenced. See
            keywords for description of this sequence and for the sequence of
            the other extremity of this insert.
FEATURES             Location/Qualifiers
     source          1. .977
                     /organism="Yarrowia lipolytica"
                     /mol_type="genomic DNA"
                     /strain="CLIB 89"
                     /db_xref="taxon:4952"
                     /clone="AW0AA029F08"
                     /clone_lib="AW0AA"
                     /note="end : T7"
     misc_feature    complement(<97. .>816)
                     /note="similar to Q23635 [ Similarity to human mucin ]"
                     /evidence=not_experimental
BASE COUNT      138 a    289 c    278 g    270 t      2 others
ORIGIN

Alignment Scores:
Pred. No.:              0.000585        Length:         977
Score:                  142.00          Matches:        83
Percent Similarity:     36.89%          Conservative:   38
Best Local Similarity:  25.30%          Mismatches:     161
Query Match:            3.31%           Indels:         46
DB:                     29              Gaps:           14

US-09-830-446-27 (1-841) x CNS06T8C (1-977)

Qy         31 SerAlaSerAsnSerPheAspGlyThrThr------SerThrThrSerPheSerSerLys 48
              |||   |||:::|||         ||||||      ||||||   |||   |||   :::
Db         29 TCTCCTTCAAGCTCTGTGACTGATACCACTCCTTCTTCCACTGGCTCTGGATCTGGCGAG 88

Qy         49 ThrSerSerAlaThrAspGlyThrAsnTyrValPheLysAspSerValValIleGluAsn 68
              :::|||||||||         |||           :::   |||
Db         89 TCCTCCTCCGCTCCTTCCTCTACTGGCGGTGCTGGCGAGTCCTCA------------ACT 136

Qy         69 ValProLysThrGlyGluThrGlnSerThrSerCysPheLysAsnAspAlaAlaAlaGly 88
                     ||||||:::   :::|||                          ||||||
Db        137 ACAGGTGGTGCTGGCGAGTCCTCTACTACT-----------------GGCGGTGCTGGC 178

Qy         89 AspLeuAsnPheLeuGlyGly---GlyPheSerPheThrPheSerAsnIle---AspAla 106
              :::   :::       ||||||   |||   |||   |||              ||:::
Db        179 GAGTCCTCTACTACTGGCGGTGCTGGTGAGTCCTCTACTACTGGTGGTGCTGGCGATTCC 238

Qy        107 ThrThrAlaSerGlyAlaAlaIleGlySerGlu------AlaAlaAsnLysThrValThr 124
              :::|||       ||||||          |||              |||   ::::::   |||
Db        239 TCTACTACTGGCGGTGCTGGTGAGTCCTCTACTACTGGCGGTGCTGGCGAGTCCTCTACT 298

Qy        125 LeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAla---SerThrValThrAsn 143
                 |||           |||                          |||:::   |||
Db        299 ACTGGCGGTGCTGGTGAGTCCTCTACTACTGGCGGTGCTGGCGAGTCCTCTACTACTGGC 358

Qy        144 GlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeu 163
              |||   |||       :::       |||
Db        359 GGTGCTGGTGAGTCCTCTACTACTGGCGGTGCTGGC---------------------- 394

Qy        164 IleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGlySerLeuLys 183
                 ::::::   :::||||||          |||       :::      |||
Db        395 ------GAGTCCTCTACTACTGGCGGTGCTGGTGAGTCCTCTACTACTGGCGGT------ 442

Qy        184 IleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArgGlyGlyAla 203
                 |||          |||   :::                 |||||||||  |||||||||
Db        443 ---GCTGGCGAGTCCTCTACTACTGGGGGTGCTGGTGAGTCCTCTACTACTGGTGGTGCT 499

Qy        204 IleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThr 223
                 :::   :::          ::::::||||||
Db        500 GGCGAGTCATCTTCTGCTCCTTCCACTACTGGTGGT--------------GCTGGCGAG 544

Qy        224 AlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSer 243
              :::   |||       |||   |||   :::                 :::|||       |||
Db        545 TCCTCCACTACTGGCGGTGCTGGTGAATCCTCCACTACTGGTGGTGCTGGCGAGTCCTCT 604

Qy        244 IleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAlaThrGlyThr 263
              :::|||   :::|||           |||   :::|||   |||       |||
Db        605 ACTACTGGCGGTGCTGGT-----------GAGTCCTCTACTACTGGCGGTGCTGGTGAG 652

Qy        264 ValSerHisSerAlaIleAspLeuGly--------------ThrSerAlaLysIleThr 278
                 |||   :::          |||                 :::||||||      |||
Db        653 TCGTCTTCTGCTCCTTCCACTACTGGTGGTGCTGGTGAGTCGTCTTCTGCTCCTTCCACT 712

Qy        279 AlaLeuArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGly 298
                    |||   :::       |||                          :::   ||||||
Db        713 ACTGGTGGTGCTGGTGAGTCCTCTACTACTGGTGGTGCTGGCGAGTCCTCTACTACTGGC 772

Qy        299 SerThrSerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGlu 318
                       :::   |||         |||   |||       ::::::
Db        773 GGTGCTGGCGAGTCCTCTGCTACCGGA---CAGTCTACTGATGGCAACAACTCCAACACC 829

Qy        319 TyrThrGlyThrIleValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGlu 338
                 ||||||          :::|||                  :::   |||
Db        830 AACACAGGCGCTTCGGAG---ACTGGTTCTAACACTGCCTCTACTACTAGCGGTGACGGT 886

Qy        339 LysAsnArgThrSerLysLeuLeu 346
                 |||       |||   ||||||
Db        887 AACAACTCTGGTTCAACACTGCTA 910

RESULT 10
CNS0768D
LOCUS       CNS0768D                1159 bp    DNA     linear   GSS 07-JUL-2001
DEFINITION  T7 end of clone BB0AA001G04 of library BB0AA from strain CBS 4732
            of Pichia angusta, genomic survey sequence.
ACCESSION   AL431075
VERSION     AL431075.1  GI:12214487
KEYWORDS    GSS.
SOURCE      Pichia angusta
  ORGANISM  Pichia angusta
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Pichia.
REFERENCE   1  (bases 1 to 1159)
  AUTHORS   Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
            Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
            de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
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            Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
            Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
            Wincker,P. and Weissenbach,J.
  TITLE     Genomic exploration of the hemiascomycetous yeasts: 1. A set of
            yeast species for molecular evolution studies
  JOURNAL   FEBS Lett. 487 (1), 3-12 (2000)
  MEDLINE   20584711
   PUBMED   11152876
REFERENCE   2  (bases 1 to 1159)
  AUTHORS   Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F.
            and Dujon,B.
  TITLE     Genomic exploration of the hemiascomycetous yeasts: 13. Pichia
            angusta
  JOURNAL   FEBS Lett. 487 (1), 76-81 (2000)
  MEDLINE   20584723
   PUBMED   11152888
REFERENCE   3  (bases 1 to 1159)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
            2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
            seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT     This GSS is part of a random genomic sequencing program of thirteen
            yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
            exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
            Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
            lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
            angusta, Debaryomyces hansenii var.  hansenii, Pichia sorbitophila,
            Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
            5 kb were prepared and both extremities were sequenced. See
            keywords for description of this sequence and for the sequence of
            the other extremity of this insert.
FEATURES             Location/Qualifiers
     source          1. .1159
                     /organism="Pichia angusta"
                     /mol_type="genomic DNA"
                     /strain="CBS 4732"
                     /db_xref="taxon:4905"
                     /clone="BB0AA001G04"
                     /clone_lib="BB0AA"
                     /note="end : T7"
BASE COUNT      255 a    408 c    230 g    260 t      6 others
ORIGIN

Alignment Scores:
Pred. No.:              0.00076       Length:         1159
Score:                  142.00        Matches:        80
Percent Similarity:     40.28%        Conservative:   63
Best Local Similarity:  22.54%        Mismatches:     147
Query Match:            3.31%         Indels:         65
DB:                     29            Gaps:           11

US-09-830-446-27 (1-841) x CNS0768D (1-1159)

Qy          11 SerLeuValProThrLeuSerMetSerAsnLeuLeuGlyAlaAlaThrThrGluGluLeu 30
               |||   :::|||:::   |||   ||||||                 :::   |||
Db         217 TCGACCTTACCGTCAGCCTCATCCTCTAAC-----------CAGGCTTCTGGCGAATCG 264

Qy          31 SerAlaSerAsnSerPheAspGlyThrThrSerThr--------------------Thr 43
               |||:::          |||::::::||||||                       |||
Db         265 TCTAGCGGAGAAATAACTACAGGGTCCAGCTCCACACAGAGCTCCCTCTCTGACTACACC 324

Qy          44 SerPheSerSerLysThrSerSerAlaThrAspGly------ThrAsnTyrValPheLys 61
               |||   ||||||   :::|||||||||||||   |||      |||      |||   :::
Db         325 TCAGCTTCCAGTGCATCCAGCAGCGCCACAACCGGCTTCTCAACTGTCACGGTGACTAGA 384

Qy          62 AspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCysPhe 81
                 |||           :::       ||||||      ||||||
Db         385 TCCTCAACACCCGATATCAGCTCTGCTCCTACTGGCAGTGCTTCCAGCACCGGAGCTAGC 444

Qy          82 LysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThrPhe 101
               ::::::   ::::::   ||||||   :::                ||||||
Db         445 GAAAGCGNCTCTTCCAACGGCGACTCTAGCCTCACAACGTCTAGTTTCTCCGGAGCCTCT 504

Qy         102 SerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsnLys 121
               ||||||:::   |||   ::::::      ::::::            ::::::
Db         505 AGCAACGTTGCTGCTCAGTCTTCTGTTGTCTCTAGCCACACAGACGCGTCCAGCCAAGTC 564

Qy         122 ThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThrVal 141
               :::   |||   |||      |||:::   |||         :::|||   :::
Db         565 TCACCAACTGACAGCTCAGGCTCTTCAACGAGCGAASCACCAGCGCCTCTAGCACCGGCC 624

Qy         142 ThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLys 161
                                    :::|||:::   :::|||:::|||      :::   :::
Db         625 TGTCGTCTGTCGTCTCCAGCCTCAGTTCGAGCTTCTCTGGCTCTTCCGACGTCACCTCAG 684

Qy         162 ValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGlySer 181
                                                                  :::   |||
Db         685 ----------------------------------------------------TCACCGTCT 693

Qy         182 LeuLysIleAlaAsnAsnLysSerLeuSerPheIleGly-AsnSerSerSerThrArgGl 201
               |||   :::|||   |||   :::::::::   :::|||    ||||||||||||
Db         694 CTT---CTGGCTACGAATGTCGCCATCACCAAGCTCGGCTACATCCTCCTCCACCATAAG 750

Qy         201 yGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGl 221
               |||          |||                                          ||
Db         751 TGGTGAACCAGATACT-------------------------------------AGCGG 771

Qy         221 yAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGlyTh 241
               |   ::::::      :::                 ::::::|||          :::||||
Db         772 AACCAGTTCAGCCGTTTCCGTGAGCTCTAGCTCGTCTGTTGCAGCTGAATCAACGGGAAC 831

Qy         241 rLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIle-------- 258
               |:::      :::|||   :::                  ||:::   :::
Db         832 AATCAAATCTGCTGGATCAGCTGCTTCGACAGAAGMAACCGGATCGCCTCTTTCCTCCTC 891

Qy         259 -------------------------GlyAlaThrGlyThrValSerHisSerAlaIleAs 270
                                        ::::::|||       |||       |||
Db         892 CAACTTCCAGACTTCTGCTCCATCGTCCAGTTCCGGCGCKACATCTTCCCAAGCCTCTGG 951

Qy         270 pLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyHisThrIleTyrPh 290
                  :::|||::::::   |||:::      |||          ::::::
Db         952 AACAGACTCCAGCTCGCAGGCTACTTCAGCCACCGCTGGTGCATCCAATTCG-------- 1003

Qy         290 eTyrAspProIleThrValThrGlySerThrSerValAlaAsp---------AlaLeuAs 307
                  |||       |||   |||   ||||||   |||:::             ||||||
Db        1004 ----GACACTCCCACAGACACACAGTCGACAGGAGTCTCTAGTTCATCTGCAGCACTACC 1059

Qy         307 nIleAsnSerProAspThrGlyAspAsnLysGluTyrThrGlyThrIleValPheSerGl 327
                ::::::|||       ||||||      :::                  |||   |||:::||
Db        1060 TGTCTCCTCG---TCTACAGGAGCTCCACGGACTYCTCTAGCACGCATC---TTCGCAGG 1113

Qy         327 yGluLysLeuThrGluAlaGluAlaLysAspGluLysAsnArg 341
               |                ::::|||              :::|||
Db        1114 AGCACCGACACTCCACGSTAAGGCAATTCGCAGAAACAGCCGG 1156

RESULT 11
BQ963411
LOCUS       BQ963411                1001 bp    mRNA    linear   EST 21-AUG-2002
DEFINITION  AGENCOURT_10055798 NIH_MGC_134 Mus musculus cDNA clone
            IMAGE:6509807 5', mRNA sequence.
ACCESSION   BQ963411
VERSION     BQ963411.1  GI:22378889
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1001)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. David Rowe
             cDNA Library Preparation: Invitrogen Corp
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            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM14077  row: k  column: 24
           High quality sequence start: 22
           High quality sequence stop: 703.
FEATURES             Location/Qualifiers
     source          1. .1001
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                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6509807"
                     /tissue_type="undifferentiated limb"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_134"
                     /note="Vector: pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2:
                     NotI; Cloned unidirectionally. Primer: Oligo dT. Average
                     insert size 1.7 kb. Constructed by ResGen, Invitrogen
                     Corp. Note: this is a NIH_MGC Library."
BASE COUNT      196 a    255 c    276 g    272 t      2 others
ORIGIN

Alignment Scores:
Pred. No.:              0.000685       Length:          1001
Score:                  141.50         Matches:           79
Percent Similarity:     36.57%         Conservative:      34
Best Local Similarity:  25.57%         Mismatches:       105
Query Match:            3.29%          Indels:            91
DB:                     13             Gaps:              14

US-09-830-446-27 (1-841) x BQ963411 (1-1001)

Qy          30 LeuSerAlaSerAsnSerPheAspGlyThrThrSerThrThrSerPheSerSerLysThr 49
               ||||||   :::   ||||||          :::|||::::::     |||
Db          24 CTCAGCACAAACACCAGCTTCGGCAGTGCACCAACTACAAGCACTGTGTTCAGTGGTGCA 83

Qy          50 SerSerAlaThrAspGlyThrAsnTyrValPheLysAspSerValValIleGluAsnVal 69
                  |||   |||   |||
Db          84 GTTAGTACCACCACTGGC---------------------------------------- 101

Qy          70 ProLysThrGlyGluThrGlnSerThrSer---CysPheLysAsnAspAlaAlaAlaGly 88
                  |||   |||   |||||||||   ||||||                    |||
Db         102 ------TTTGGAGGCACACTTAGCACCAGTGTCTGCTTT-----------------GGT 137

Qy          89 AspLeuAsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThr 108
                  :::   |||   ||||||      |||   |||
Db         138 AGTTCTCCCTACTCTGGCGCTGGCTTTGGAGGCACACTTAGT----------------- 179

Qy         109 AlaSerGlyAlaAlaIleGlySerGluAlaAlaAsnLysThrValThrLeuSerGlyPhe 128

Db         179 ------------------------------------------------------------ 179

Qy         129 SerAlaLeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIle 148
               :::::::::||||||      ||||||::::::          |||   |||
Db         180 ACCAGTATCTCCTTTGGTGGTTCTCCTAGCACC------AATACTGGTTTTGGT------ 227

Qy         149 AsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsnPhe 168
                  |||   ||||||              |||                   :::
Db         228 ---------GGTACACTCAGC-----------ACCAGTGTTTCCTTCGGTGCTTCTTCT 266

Qy         169 SerThrGlyAsp------GlyGlyAlaIleAsnCysAlaGlySerLeuLysIleAlaAsn 186
               ||||||            ||||||   ::::::   :::   |||          ::::::
Db         267 AGCACCAGCTCTGACTTTGGTGGCACACTAAGCACTAGTGTCAGCTTTGGTGGCTCTTCT 326

Qy         187 AsnLysSerLeuSerPheIleGly------AsnSerSerSerThrArgGlyGlyAlaIle 204
                  :::      |||   |||        |||||||||::::::   ||||||||||||
Db         327 GGTGCCAATGCTGGCTTTGGCGGTACACTCAACAGCAGTACCAGCTTTGGCGGTGCCATC 386

Qy         205 HisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAla 224
               |||                  |||:::|||              |||:::
Db         387 AGCACC--------------AGCACTGGC--------------TTTGGCAGTGCACTC 416

Qy         225 ProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIle 244
                  :::|||    ||||||||||||:::   :::   ||||||   |||:::
Db         417 AATAACAGTGCCAACTTTGGTGGTGCCATAAGTACCAGCTTTAGTGGTGTACTCAATAGC 476

Qy         245 SerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAlaThrGlyThrVal 264
               |||          |||      |||         ||||||            |||:::
Db         477 AGTGCCAGCTTTGGTGGTGCCATC---------AACACCAGTGCTGGCTTCGGCAGTACA 527

Qy         265 SerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGln 284
                  :::|||:::         |||::::::        :::|||
Db         528 CTCAACAGCAGTGCCAGCTTTGGCAGTGCACTCAGCACCAGTGCCAGCTTTGGTGGT--- 584

Qy         285 GlyHisThrIleTyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAsp 304
                                                  :::   ||||||
Db         585 ----------------------------GTACTCAATGGCAGTGCTGGCTTTGGTGGT 614

Qy         305 AlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGluTyrThrGlyThrIleVal 324
               |||||||||   |||:::         |||                  |||:::
Db         615 GCCTTGAACACCAATGCCACCTTTGGTGGT---------GTACTCAATGGCAGTGCTGGC 665

Qy         325 PheSerGlyGluLysLeuThrGluAla 333
               |||   |||          |||   |||
Db         666 TTTGGTGGTGCCATGAACACCAATGCC 692

RESULT 12
BE583883
LOCUS       BE583883                634 bp    mRNA    linear   EST 16-AUG-2000
DEFINITION  8-11G-HA PsojaeHA Glycine max/Phytophthora sojae mixed EST library
            cDNA, mRNA sequence.
ACCESSION   BE583883
VERSION     BE583883.1  GI:9834832
KEYWORDS    EST.
SOURCE      Glycine max/Phytophthora sojae mixed EST library
  ORGANISM  Glycine max/Phytophthora sojae mixed EST library
            Eukaryota; mixed EST libraries.
REFERENCE   1  (bases 1 to 634)
  AUTHORS   Qutob,D., Hraber,P.T., Sobral,B.W.S. and Gijzen,M.
  TITLE     Comparative analysis of expressed sequences in Phytophthora sojae
  JOURNAL   Plant Physiol. 123 (1), 243-254 (2000)
  MEDLINE   20267956
   PUBMED   10806241
COMMENT     Contact: Gijzen M
            Agriculture and Agri-Food Canada
            1391 Sandford Street, London, Ontario, Canada N5V 4T3
            Tel: 519 457 1470
            Fax: 519 457 3997
            Email: gijzenm@em.agr.ca
            Transcript obtained from mixed plant-pathogen interaction culture.
FEATURES             Location/Qualifiers
     source          1. .634
                     /organism="Glycine max/Phytophthora sojae mixed EST
                     library"
                     /mol_type="mRNA"
                     /strain="Phytophthora sojae race 2 strain P6497"
                     /cultivar="Glycine max cultivar Harosoy"
                     /db_xref="taxon:135715"
                     /tissue_type="Plant hypocotyls infected with Phytophthora
                     sojae"
                     /dev_stage="8 d old etiolated hypocotyls 48 h
                     post-inoculation with Phytophthora sojae zoospores"
                     /lab_host="E. coli strain XLOLR"
                     /clone_lib="PsojaeHA"
                     /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; This
                     cDNA library was constructed from polyA+ enriched mRNA
                     from etiolated  hypocotyls 48 h post-inoculation with
                     Phytophthora sojae zoospores.  Complementary DNA was
                     synthesized from mRNA using an XhoI-poly(dT)
                     linker-primer. EcoRI adapters were ligated to the
                     blunt-ended cDNA  fragments and the products were digested
                     with XhoI for directional cloning  into lambda ZAP Express
                     vector. This lambda library was amplified once  using E.
                     coli host strain XL1 Blue MRF'. Inserts were then
```

```
                    subcloned  by mass excision using ExAssist helper phage
                    for conversion into phagemid  vector pBK-CMV in E. coli
                    host strain XLOLR.  Sequenced using T3 primer: 5' ATT AAC
                    CCT CAC TAA AGG GA 3'."
BASE COUNT      146 a    227 c    182 g     78 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:              0.000434       Length:         634
Score:                  140.50         Matches:        66
Percent Similarity:     35.31%         Conservative:   35
Best Local Similarity:  23.08%         Mismatches:     94
Query Match:            3.27%          Indels:         91
DB:                     10             Gaps:           13

US-09-830-446-27 (1-841) x BE583883 (1-634)

Qy         31 SerAlaSerAsnSerPheAspGlyThrThrSerThrThrSerPheSerSerLysThrSer 50
              :::::::::||||||      ||||||::::::|||   |||   ::::::   ||||||
Db          6 ACCTCGACCAACTCT------GGTACCTCGACCACGAACTCGGGTACGACCTCGACTTCG 59

Qy         51 SerAlaThrAspGlyThrAsnTyrValPheLysAspSerValValIleGluAsnValPro 70
              :::   |||   ||||||
Db         60 ACCACCACCGGCGGCACTACC------------------------------------- 80

Qy         71 LysThrGlyGluThrGlnSerThrSerCysPheLysAsnAspAlaAlaAlaGlyAspLeu 90
                 :::|||   |||   ||||||:::          :::
Db         81 AGCTCCGGCACCACTTCGTCCACTACGAGCGGAAACACCAGCTCGGGTACGACCTCGACC 140

Qy         91 AsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThrAlaSer 110
              |||           |||   :::   |||   :::           ||||||:::|||
Db        141 AAC---------TCTGGTACGACCTCGACTTCGACTACCACGGGCGGAACCACGAGCTCC 191

Qy        111 GlyAlaAlaIleGlySerGluAlaAlaAsnLysThrValThrLeuSerGlyPheSerAla 130
              |||                              :::   |||   ||||||   |||
Db        192 GGT--------------------ACGACTTCGTCCACCACGAACTCGGGCACGTCCACC 230

Qy        131 LeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIleAsnVal 150
                 |||                 :::||||||   |||   |||
Db        231 ---TCAACGACGACCGGCGGCAGCTCGACGACTACCACGGGC----------------- 269

Qy        151 LysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsnPheSerThr 170
                                                        |||         :::|||
Db        270 ----------------------------------------CAGACGACGACGGCCACG 287

Qy        171 GlyAspGlyGly---------AlaIleAsnCysAlaGlySerLeuLysIleAlaAsnAsn 187
              |||     |||                          ||||||          |||
Db        288 GGCTCGAACGGTGAGACGATCACGACTACCACGACGGGCTCG-----------AACGGC 335

Qy        188 LysSerLeuSerPheIleGlyAsnSerSerSerThrArgGlyGlyAlaIleHisThrLys 207
              :::::::::                :::::::::|||   |||           |||
Db        336 GAGACGATC--------------ACGACTACCACGACGGGCTCGAACGGCGAGACGATC 380

Qy        208 AsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaProThrAla 227
                 |||     |||   ||||||                  |||     |||
Db        381 ACGACGACGACTGGCTCGAGCGGTGAG--------------AAGACCACTACCACGACG 425

Qy        228 AlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAsp 247
                 |||   ||||||:::::   :::   ::::::|||:::
Db        426 ACGGGTTCGGGTGGCTCTGTTCAGGTCACGGAGACCGGATCG----------------- 467

Qy        248 SerGlyAspIleIlePheGluGlyAsnThrIleGlyAlaThrGlyThrValSerHisSer 267
                                  |||   :::|||     |||   |||
Db        468 --------------------GGCGGCTCCATTGAGACCACGACGACG------------ 494

Qy        268 AlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyHisThr 287
                       |||:::   |||       |||   :::             |||   :::
Db        495 ------------GGCTCGGGAGCCACGACGACGACGGTCACCACGGGCTCGGGTGCCTCG 542

Qy        288 IleTyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsn 307
                                  |||   |||       ||||||          :::   |||
Db        543 --------------------ACTACGACGACGGGCACTAGCACGTNCACCTCGACGAAC 581
```

```
Qy         308 IleAsnSerProAspThr 313
                     :::|||   |||
Db         582 TCTGGCAACCCCACGACT 599

RESULT 13
CA318878
LOCUS       CA318878                779 bp    mRNA    linear   EST 26-NOV-2002
DEFINITION  UI-M-FW0-cbr-j-23-0-UI.r1 NIH_BMAP_FW0 Mus musculus cDNA clone
            IMAGE: 6813528 5', mRNA sequence.
ACCESSION   CA318878
VERSION     CA318878.1  GI:24537002
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 779)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1. .779
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE: 6813528"
                     /tissue_type="whole brain"
                     /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_FW0"
                     /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site. Double strand cDNA was
                     size selected according to mRNA size fraction, ligated
                     with EcoR I adaptor, digested with NotI and then cloned
                     directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is AGCGAGACAG. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                     program coordinator."
BASE COUNT      154 a    209 c    203 g    212 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:              0.000671       Length:         779
Score:                  140.00         Matches:        80
Percent Similarity:     38.19%         Conservative:   38
Best Local Similarity:  25.89%         Mismatches:     108
Query Match:            3.26%          Indels:         83
DB:                     14             Gaps:           15

US-09-830-446-27 (1-841) x CA318878 (1-779)

Qy          31 SerAlaSerAsnSerPheAspGlyThrThrSerThrThrSerPheSerSerLysThrSer 50
               |||   :::      |||         ::::::   |||||||||   |||      ::::
```

```
Db         24 AGTACCAACCCTGGCTTTAGTGCACTCAGCACAAACACCAGCTTCGGCAGTGCACCAACT 83

Qy         51 SerAlaThrAspGlyThrAsnTyrValPheLysAspSerValValIleGluAsnValPro 70

Db         84 ACAAGCACT--------------GTGTTC------AGTGGTGCAGTTAGTACCACCACT 122

Qy         71 LysThrGlyGluThrGlnSerThrSer---CysPheLysAsnAspAlaAlaAlaGlyAsp 89

Db        123 GGCTTTGGAGGCACACTTAGCACCAGTGTCTGCTTT-----------------GGTAGT 164

Qy         90 LeuAsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThrAla 109

Db        165 TCTCCCTACTCTGGCGCTGGCTTTGGAGGCACACTTAGT--------------------- 203

Qy        110 SerGlyAlaAlaIleGlySerGluAlaAlaAsnLysThrValThrLeuSerGlyPheSer 129

Db        204 ------------------------------------------------------ACC 206

Qy        130 AlaLeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIleAsn 149

Db        207 AGTATCTCCTTTGGTGGCTCTCCTAGCACC------AATACTGGTTTTGGT--------- 251

Qy        150 ValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsnPheSer 169

Db        252 ------GGTACACTCAGC------------ACCAGTGTTTCCTTCGGTGCTTCTTCTAGC 293

Qy        170 ThrGlyAsp------GlyGlyAlaIleAsnCysAlaGlySerLeuLysIleAlaAsnAsn 187

Db        294 ACCAGCTCTGACTTTGGTGGCACACTAAGCACTAGTGTCAGCTTTGGTGGCTCTTCTGGT 353

Qy        188 LysSerLeuSerPheIleGly------AsnSerSerSerThrArgGlyGlyAlaIleHis 205

Db        354 GCCAATGCTGGCTTTGGCGGTACACTCAACAGCAGTACCAGCTTTGGCGGTGCCATCAGC 413

Qy        206 ThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaPro 225

Db        414 ACC---------------AGCACTGGC--------------TTTGGCAGTGCACTCAAT 443

Qy        226 ThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSer 245

Db        444 AACAGTGCCAACTTTGGTGGTGCCATAAGTACCAGCTTTAGTGGTGTACTCAATAGCAGT 503

Qy        246 GlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAlaThrGlyThrValSer 265

Db        504 GCCAGCTTTGGTGGTGCCATC---------AACACCAGTGCTGGCTTCGGCAGTACACTC 554

Qy        266 HisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGly 285

Db        555 AACAGCAGTGCCAGCTTTGGCAGTGCACTCAGCACCAGTGCCAGCTTTGGTGGT------ 608

Qy        286 HisThrIleTyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAla 305

Db        609 -------------------------GTACTCAATGGCACTGCTGGCTTTGGTGGTGCC 641

Qy        306 LeuAsnIleAsnSer-ProAspThrGlyAspAsnLysGluTyrThrGlyThrIleValPh 325

Db        642 TTGAACACCAATGCCACCTNTTGGTGGT---------GTACTCAATGGCAGTGCTGGCTT 692

Qy        325 eSerGlyGluLysLeuThrGluAla 333

Db        693 TGGTGGTGCCATGAACACCAATGCA 717

RESULT 14
BJ368874
LOCUS       BJ368874                 788 bp    mRNA    linear   EST 08-MAR-2002
DEFINITION  BJ368874 Dictyostelium discoideum cDNA library, CF Dictyostelium
            discoideum cDNA clone ddc48l10 5', mRNA sequence.
ACCESSION   BJ368874
VERSION     BJ368874.1  GI:19278257
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 788)
  AUTHORS   Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
  TITLE     Full length cDNA of Dictyostelium discoideum at the culmination
            stage
  JOURNAL   Unpublished
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .788
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="ddc48l10"
                     /sex="mat A"
                     /dev_stage="Culmination stage"
                     /clone_lib="Dictyostelium discoideum cDNA library, CF"
BASE COUNT      245 a    168 c    170 g    198 t      7 others
ORIGIN

Alignment Scores:
Pred. No.:                0.00125        Length:          788
Score:                    137.50         Matches:         78
Percent Similarity:       36.40%         Conservative:    25
Best Local Similarity:    27.56%         Mismatches:      115
Query Match:              3.20%          Indels:          65
DB:                       12             Gaps:            13

US-09-830-446-27 (1-841) x BJ368874 (1-788)

Qy         64 ValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCysPheLysAsn 83

Db         27 ATAATGTCAAACAATTTATTTGGTACAGGTTCATCAACTTCATCATCATTATTTGGTTCA 86

Qy         84 AspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr--------- 100

Db         87 ACACCTTCAGCAGGTGGATTA------TTTGGTGGTGGTAGTTCAACAACACCAGCAACA 140

Qy        101 ---------------PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGly 115

Db        141 GGCGGTGGTGGTTTATTTGGAGGTGCCTCAACAACACCAGCAACAGGCGGCGGTTTATTT 200

Qy        116 SerGluAlaAlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLys 135

Db        201 GGAGGTGCCTCAACAACACCAGCAACAGGTGGTGGT-----------------TTATTT 242

Qy        136 SerProAlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSer 155

Db        243 GGAGGTGCCTCAACA---ACACCAGCAACAGGTGGTGGTGGTTTATTTGGAGGTAGTAGC 299

Qy        156 LeuLeuAspAsnAspLysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAla 175

Db        300 ACTACAGCACCA------------------------GCAACAGGTGGTGGTGGTTTA 332

Qy        176 IleAsnCysAlaGlySerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsn 195

Db        333 TTT------GGTGGTTCTACAACAACTGCACCAGCAACTACTGGAGGATTATTTGGAGGT 386

Qy        196 SerSerSerThrArg-------------------------GlyGlyAlaIleHisThr 206

Db        387 AGTAGCACTACAGCACCATCAACAACAACTGGTGGATTATTCGGAGGTTCTTCAACAACT 446

Qy        207 LysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGly------AsnThrAla 224

Db        447 ACACCATCAATAACAACAACAGGAGGA------TTATTTGGAGGTGCTTCAACAACTGCA 500

Qy        225 Pro------ThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGlyThrLeu 242
```

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Db        501 CCATCAACAACAACAGGTGGATTATTTGGAGCAACTACACCAGCAACTACAGCAACAACA 560

Qy        243 SerIleSerGly--------------------------------AspSerGlyAspIle 251
              :::     |||                                 ||||||
Db        561 ACAACAGGTGGATTATTTGGCGGATCTACAACCACACCATCATTAACAAGTGGTGGAGGT 620

Qy        252 IlePheGluGlyAsnThrIleGlyAlaThrGlyThrValSerHisSerAlaIleAspLeu 271
              :::|||     |||     ||||||  |||  :::  |||||||||
Db        621 TTATTTGGAGCAACTACACCAGCAGCTACAACAACAACAACATCCTCAGCTATACCATCA 680

Qy        272 GlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyHisThrIleTyrPheTyr 291
                ||:::                          |||      :::|||||
Db        681 TTAACTACC----------------------------GGNGGGANGGTTTATTTTGGN 710

Qy        292 AspProIleThrValThrGlySerThrSerValAlaAspAlaLeu---AsnIleAsnSer 310
                  |||           |||:::     |||  |||     :::
Db        711 GGATCTACAACTACACCATCATTAACTAATGGGNGGGATTATTTGGAGCAACTACNCCAN 770

Qy        311 ProAspThr 313
              |||  |||
Db        771 CCANCTACA 779

RESULT 15
CD284689/c
LOCUS       CD284689                698 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  G39178.95 NCI_CGAP_ZKid1 Danio rerio cDNA clone IMAGE:6524567 5',
            mRNA sequence.
ACCESSION   CD284689
VERSION     CD284689.1  GI:31062465
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 698)
  AUTHORS   Amundsen,C., Cachuela,N., Chen,F., Cheung,L.M., Chong,A., Murray,L.
            , Oliva,J., Park,C., Reyes,J., Yungen,J. and Swimmer,C.
  TITLE     Expressed sequence tags from NCI_CGAP_ZKid1, a Danio rerio kidney
            library
  JOURNAL   Unpublished
COMMENT     Contact: Chen F.
            Exelixis, Inc.
            170 Harbor Way, PO Box 511, South San Francisco, CA 94083-0511, USA
            Tel: 650 837 7000
            Fax: 650 837 8300
            Email: fchen@exelixis.com
            DNA Sequencing by: Exelixis, Inc. Clone distribution information
            can be found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: 14116  row: N  column: 23
            High quality sequence stop: 698.
FEATURES             Location/Qualifiers
     source          1. .698
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:6524567"
                     /lab_host="DH10B (T1-resistant)"
                     /clone_lib="NCI_CGAP_ZKid1"
                     /note="Organ: kidney; Vector: pCMV-SPORT6.ccdb; Site_1:
                     EcoRV; Site_2: NotI; Cloned unidirectionally. Primer:
                     Oligo dT. Average insert size 1.8 kb. Constructed by J.
                     Wang (Research Genetics, Invitrogen Corp) from tissue
                     donated by L. Zon (Harvard University). Note: this is a
                     NCI_CGAP Library."
BASE COUNT      226 a    186 c    182 g    104 t
ORIGIN

Alignment Scores:
Pred. No.:              0.00168         Length:         698
Score:                  135.50          Matches:        79
Percent Similarity:     35.74%          Conservative:   30

Best Local Similarity:  25.90%          Mismatches:     103
Query Match:            3.15%           Indels:         93
DB:                     14              Gaps:           15

US-09-830-446-27 (1-841) x CD284689 (1-698)

Qy         25 AlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThrSerThrThrSer 44
              :::||||||      ::|||   |||                 :::         :::
Db        698 TCTACTACTTCCTCTGTGACTGGTTCCACTGGTGAAGCTGCAAGTTGAGGTGACAGTGGA 639

Qy         45 PheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPheLysAspServal 64
                ||||||  :::   :::|||:::  |||                  ||||||
Db        638 GGCTCCTCAGGCTCATGTGCAGCATCCTCAGGTGCAACT---------GCAGATTCC--- 591

Qy         65 ValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCysPheLysAsnAsp 84
                                  :::|||  |||  |||:::|||
Db        590 ---------------TCAGCCTCAGGGGCGACTGTGTCTTCTTCA-----------GGT 558

Qy         85 AlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIle 104
              ||||||||||||  |||:::           |||  |||  :::  :::
Db        557 GCAGCAGCAGGTGTCTTGTCC---ACTGCTGATGGAATCTCAGAAAGTGTTACAGGTTCC 501

Qy        105 AspAlaThrThrAlaSerGlyAlaAlaIleGlySerGlu---------------------- 117
                ||||||  ||||||||:::|||      |||
Db        500 TCTGCCACTGGTGCTTCTGGCTCAGCTGCTAGTTCTTCATGTGTAGCTGGAGGTTCTTCT 441

Qy        118 -----------------AlaAlaAsnLysThrValThrLeuSerGlyPheSerAlaLeu 131
                              ||||||     :::|||      :::|||||||||
Db        440 TTAACTGGTGTCTCAGGAGCAGCAACTGGTTCTGTTGCAACCACTGGTTTCTCC------ 387

Qy        132 SerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValLys 151
                 :::        :::  |||||||||  |||
Db        386 ------ATCACTGGTGACTCTGGTACTGTAACTGCAGGTTCCTCCACTACTGGTGCAGCT 333

Qy        152 GlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsnPheSerThrGly 171
                  |||                                  |||   ||||||
Db        332 GCTGGTTCTTCA--------------------------------GGTTTTTTAACTGGT 306

Qy        172 AspGlyGlyAlaIle---------AsnCysAlaGlySerLeuLysIleAlaAsnAsnLys 188
              |||   ||||||           :::   ||||||||||||      |||
Db        305 GACTCTGGTGCAGCTGCAGGCTCCTCAGCTGCTGGTTCTTTAGGTGCCGCT--------- 255

Qy        189 SerLeuSerPheIleGlyAsnSerSerSerThrArgGlyGlyAlaIleHisThrLysAsn 208
                          |||:::  ::::::|||     |||
Db        254 -----------GCAGGCTCTGGCACAGCTACTGCAGCTGGT----------------- 225

Qy        209 LeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAla 228
                        ||||||      |||      ||||||   |||:::|||
Db        224 -----------TCTGGTGCAGCTGCTGCTTTCTCTTCAACAACTGCTGTTACCTCTGCA 177

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Qy        249 GlyAspIleIlePheGluGlyAsnThrIleGlyAlaThrGlyThrValSerHisSerAla 268
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Db        155 ------------------------------------GCTGTTGTCTCTACTGCTGCT 135

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Qy        287 ThrIleTyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeu 306
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Db         74 GGAGTAGATGTC------TCTGTGGTTGCCACTGGTTCTTCTAGTGCAGCATCATCCTTC 21

Qy        307 AsnIleAsnSerPro 311
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Db         20 ---TTTACCTCTCCT 9


Search completed: January 29, 2004, 17:50:08
Job time : 4279 secs
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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 29, 2004, 10:21:11 ; Search time 121 Seconds
(without alignments)
3067.795 Million cell updates/sec

Title: US-09-830-446-27
Perfect score: 4295
Sequence: 1 MKIPLRFLLISLVPTLSMSN.....FEWRGSSRSYNVDAGSKIKF 841

Scoring table: BLOSUM62
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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4255	99.1	1230025	4	US-09-198-452A-1	Sequence 1, Appli
c 2	1365	31.8	1230025	4	US-09-198-452A-1	Sequence 1, Appli
3	939	21.9	3021	4	US-09-556-877-182	Sequence 182, App
4	939	21.9	3021	4	US-09-620-412C-182	Sequence 182, App
5	939	21.9	3021	4	US-09-598-419-182	Sequence 182, App
6	936	21.8	2949	4	US-09-556-877-170	Sequence 170, App
7	936	21.8	2949	4	US-09-620-412C-170	Sequence 170, App
8	936	21.8	2949	4	US-09-598-419-170	Sequence 170, App
9	711.5	16.6	2643	4	US-09-556-877-169	Sequence 169, App
10	711.5	16.6	2643	4	US-09-620-412C-169	Sequence 169, App
11	711.5	16.6	2643	4	US-09-598-419-169	Sequence 169, App
12	696.5	16.2	2601	4	US-09-556-877-181	Sequence 181, App
13	696.5	16.2	2601	4	US-09-620-412C-181	Sequence 181, App
14	696.5	16.2	2601	4	US-09-598-419-181	Sequence 181, App
15	527.5	12.3	2895	4	US-09-556-877-171	Sequence 171, App
16	527.5	12.3	2895	4	US-09-620-412C-171	Sequence 171, App
17	527.5	12.3	2895	4	US-09-598-419-171	Sequence 171, App
18	527.5	12.3	2934	4	US-09-556-877-183	Sequence 183, App
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35	421	9.8	2847	4	US-09-598-419-186	Sequence 186, App
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38	333	7.8	2076	4	US-09-620-412C-312	Sequence 312, App
39	333	7.8	2076	4	US-09-598-419-312	Sequence 312, App
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41	290	6.8	2148	4	US-09-598-419-328	Sequence 328, App
42	266	6.2	1965	4	US-09-620-412C-340	Sequence 340, App
43	266	6.2	1965	4	US-09-598-419-340	Sequence 340, App
44	266	6.2	2052	4	US-09-620-412C-356	Sequence 356, App
45	266	6.2	2052	4	US-09-598-419-356	Sequence 356, App

ALIGNMENTS

RESULT 1
US-09-198-452A-1
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
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Best Local Similarity:	99.76%	Mismatches:	1
Query Match:	99.07%	Indels:	2
DB:	4	Gaps:	0

US-09-830-446-27 (1-841) x US-09-198-452A-1 (1-1230025)

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Qy        121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
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Qy        201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220
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Db      30269 CTTTTTGAATGAGGACCATTCCTATGATGGGATTCTTGAGTTAGATGCTGGGAAAGACAT 30328

Qy        460 eValIleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGl 480
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Db      30329 CGTGATTTCTGCAGATTCTCGCAGTATAGATGCTGTACAATCTCCGTATGGCTATCAGGG 30388

Qy        480 yLysTrpThrIleAsnTrpSerThrAspAspLysLysAlaThrValSerTrpAlaLysGl 500
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Db      30389 AAAGTGGACGATCAATTGGTCTACTGATGATAAGAAAGCTACGGTTTCTTGGGCGAAGCA 30448

Qy        500 nSerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySe 520
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Db      30449 GAGTTTTAATCCCACTGCTGAGCAGGAGGCTCCGTTAGTTCCTAATCTTCTTTGGGGTTC 30508

Qy        520 rPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTy 540
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Db      30509 TTTTATAGATGTTCGTTCCTTCCAGAATTTTATAGAGCTAGGTACTGAAGGTGCTCCTTA 30568

Qy        540 rGluLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAs 560
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Db      30569 CGAAAAGAGATTTTGGGTTGCAGGCATTTCCAATGTTTTGCATAGGAGCGGTCGTGAAAA 30628

Qy        560 nGlnArgLysPheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArgMetPr 580
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Db      30629 TCAAAGGAAATTCCGTCATGTGAGTGGAGGTGCTGTAGTAGGTGCTAGCACGAGGATGCC 30688
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Qy        600 eMetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSe 620
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Qy        620 rLeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuPr 640
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Qy        640 oTyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAs 660
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Qy        680 rSerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAlaValGluAsnTh 700
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Qy        700 rSerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGlnAlaValTyrAl 720
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Qy        840 sPhe 841
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Db      31469 ATTT 31472

RESULT 2
US-09-198-452A-1/c
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/09/198,452A
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
;   LENGTH: 1230025
;   TYPE: DNA
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Alignment Scores:

Pred. No.:	1.28e-132	Length:	1230025
Score:	1365.00	Matches:	329
Percent Similarity:	51.04%	Conservative:	161
Best Local Similarity:	34.27%	Mismatches:	320
Query Match:	31.78%	Indels:	151
DB:	4	Gaps:	22

US-09-830-446-27 (1-841) x US-09-198-452A-1 (1-1230025)

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Qy          1 MetLysIleProLeuArgPheLeuLeuIle---SerLeuValProThrLeuSerMetSer 19
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Db     518200 ATGAAATCGCAATTTTCCTGGTTAGTGCTCTCTTCGACATTGGCATGTTTTACTAGTTGT 518141

Qy         20 AsnLeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThr 39
              :::   :::   |||||||||   |||   :::      |||:::|||||||||||:::
Db     518140 TCCACTGTTTTTGCTGCAACTGCTGAAAATATAGGCCCCTCTGATAGCTTTGACGGAAGT 518081

Qy         40 ThrSerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrVal 59
              |||:::|||   :::::::::   |||      :::   |||   |||   :::|||
Db     518080 ACTAACACAGGCACCTATACTCCTAAA------AATACGACTACTGGAATAGACTATACT 518027

Qy         60 PheLysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSer 79
                        :::   ::::::|||:::          |||::::::   :::   :::
Db     518026 CTGACAGGAGATATAACTCTGCAAAACCTT---------GGGGATTCGGCAGCTTTAACG 517976

Qy         80 ------CysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPhe 97
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Db     517975 AAGGGTTGTTTTTCTGACACTACGGAATCT------TTAAGCTTTGCCGGTAAGGGGTAC 517922

Qy         98 SerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGlu 117
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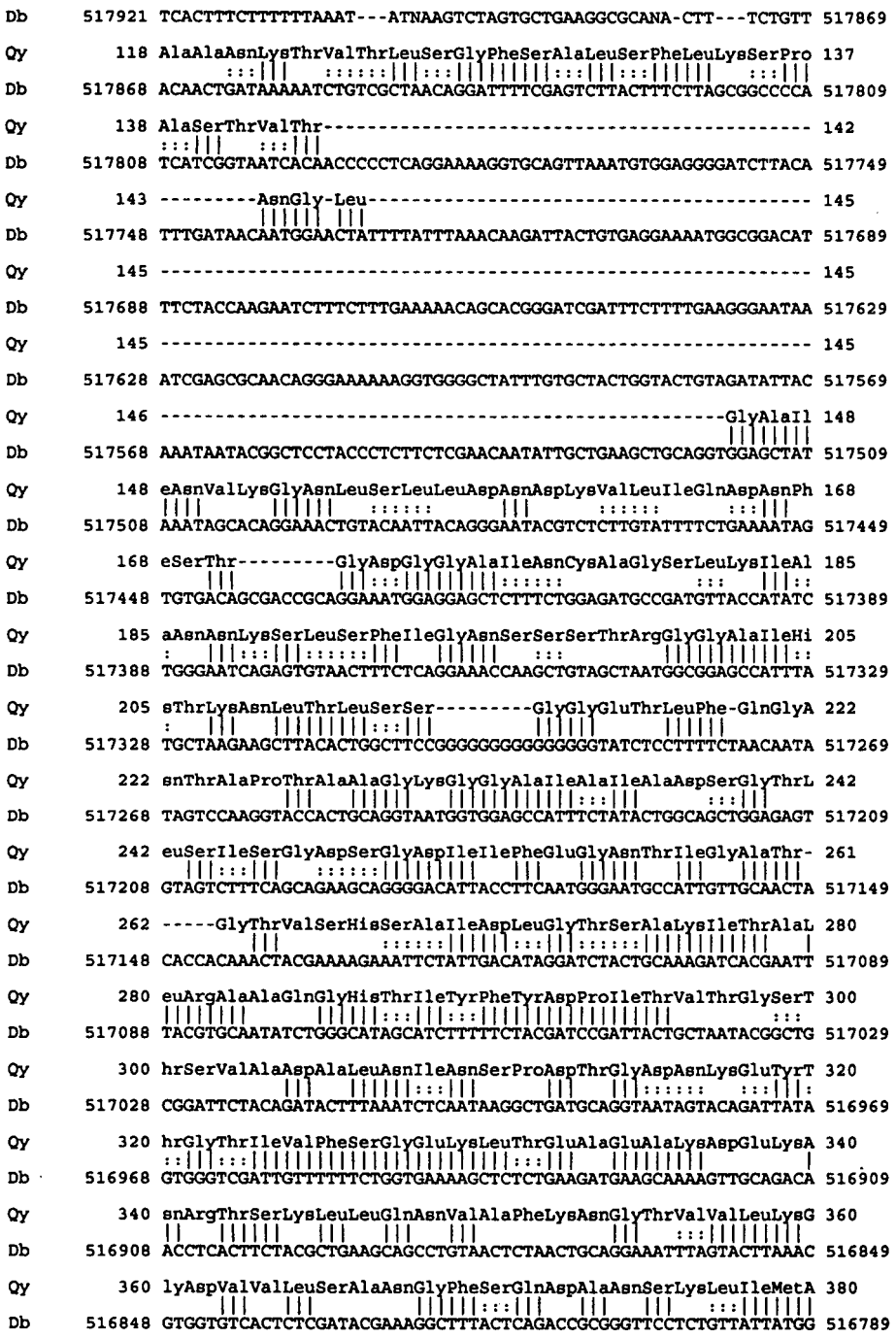
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RESULT 3
US-09-556-877-182
; Sequence 182, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
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; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
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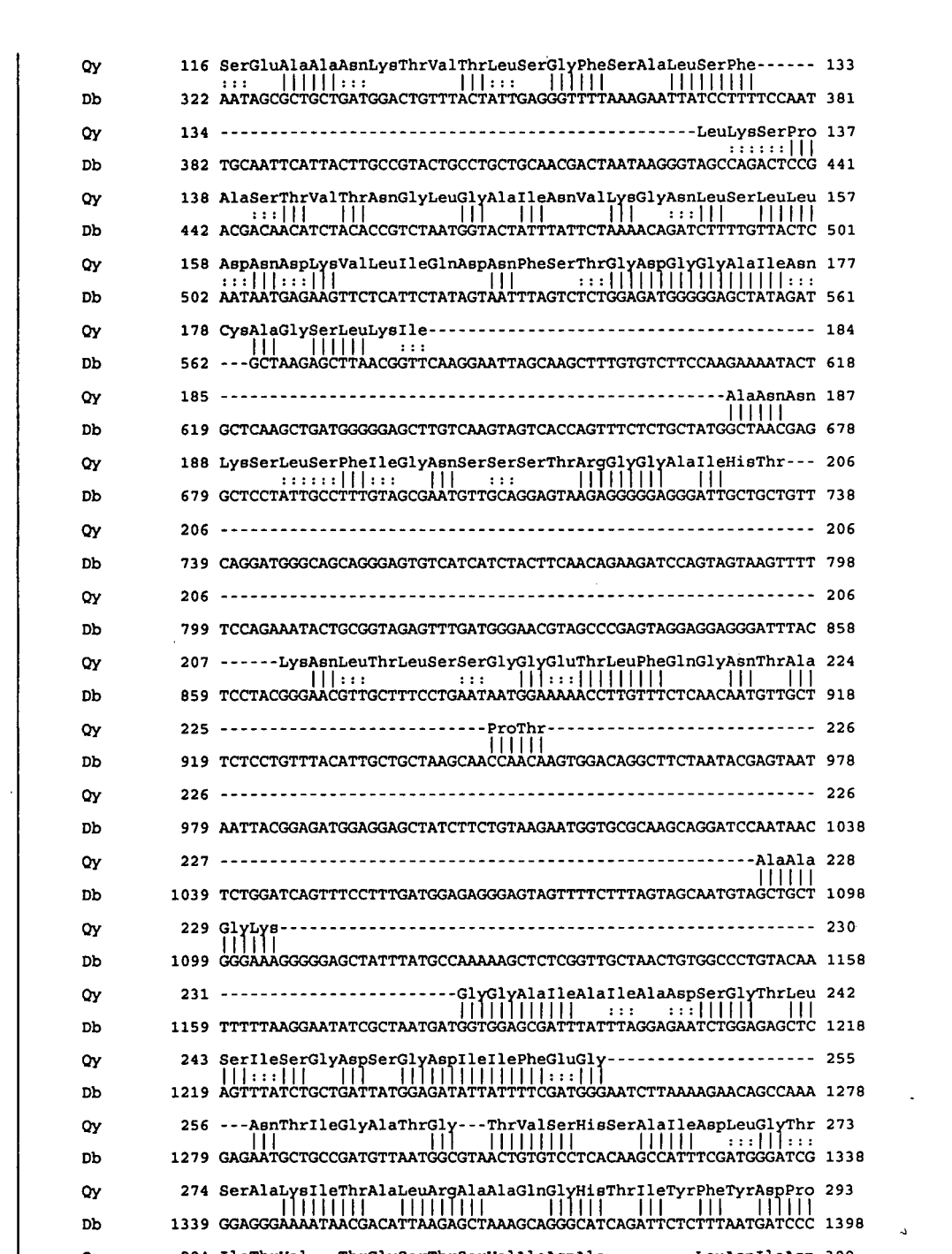
US-09-556-877-182

Alignment Scores:

Pred. No.:	5.22e-91	Length:	3021
Score:	939.00	Matches:	285
Percent Similarity:	39.77%	Conservative:	127
Best Local Similarity:	27.51%	Mismatches:	334
Query Match:	21.86%	Indels:	290
DB:	4	Gaps:	29

US-09-830-446-27 (1-841) x US-09-556-877-182 (1-3021)



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Db       1399 ATCGAGATGGCAAACGGAAATAACCAGCCAGCGCAGTCTTCCAAACTTCTAAAAATTAAC 1458

Qy        310 SerProAspThrGlyAspAsnLysGluTyrThrGlyThrIleValPheSerGlyGluLys 329

Db       1459 --------------GATGGTGAAGGATACACAGGGGATATTGTTTTTGCT--------- 1494

Qy        330 LeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSerLysLeuLeuGlnAsnVal 349

Db       1495 ----------------------------AATGGAAGCAGTACTTTGTACCAAAATGTT 1524

Qy        350 AlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsnGlyPhe 369

Db       1525 ACGATAGAGCAAGGAAGGATTGTTCTTCGTGAAAAGGCAAAATTATCAGTGAATTCTCTA 1584

Qy        370 SerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeu------------ 385

Db       1585 AGTCAGACAGGTGGGAGT---CTGTATATGGAAGCTGGGAGTACATTGGATTTTGTAACT 1641

Qy        386 ----------------------ValAlaAsnThrGluSerIleGluLeuThrAsnLeuGlu 398

Db       1642 CCACAACCACCACAACAGCCTCCTGCCGCTAATCAGTTGATCACGCTTTCCAATCTGCAT 1701

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Qy        411 ------------------LysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAsp 424

Db       1762 GCGCAAGATTCTCATCCTGCAGTCATTGGTAGCACAACTGCTGGTTCTGTTACAATTAGT 1821

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Db       1822 GGGCCTATCTTTTTTGAGGATTTGGATGATACAGCTTATGATAGG--------------- 1866

Qy        445 AspHisSerTyrAsp------------------------GlyIleLeuGluLeuAspAla 456

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Qy        476 TyrGlyTyrGlnGlyLysTrpThrIleAsnTrpSerThrAspAspLys------------ 491

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Db       2152 TCAGCAATTCAAGCAAGTGTGGATGGGCGCTCTTATTGTCGAGGATTATGGGTTTCTGGA 2211

Qy        549 IleSerAsnValLeuHisArgSerGlyArgGluAsnGlnArgLysPheArgHisValSer 568

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Qy        569 GlyGlyAlaValValGlyAlaSerThrArgMetProGlyGlyAspThrLeuSerLeuGly 588

Db       2272 GGGGGTTATTCCTTAGGAGCAAACTCCTACTTT---GGATCATCGATGTTTGGTCTAGCA 2328

Qy        589 PheAlaGlnLeuPheAlaArgAspLysAspTyrPheMetAsnThrAsnPheAlaLysThr 608

Db       2329 TTTACCGAAGTATTTGGTAGATCTAAAGATTATGTAGTGTGTCGTTCCAATCATCATGCT 2388

Qy        609 TyrAlaGlySerLeuArgLeuGlnHisAspAlaSerLeuTyrSerValValSerIleLeu 628

Db       2389 TGCATAGGATCCGTTTATCTATCTACCCAACAAGCTTTATGTGGA------TCCTATTTG 2442

Qy        629 LeuGlyGluGlyGlyLeuArgGluIleLeuLeuProTyrValSerLysThrLeuProCys 648

Db       2443 TTCGGAGATGCGTTTATCCGT---------------------------------------- 2463

Qy        649 SerPheTyrGlyGlnLeuSerTyrGlyHisThrAspHisArgMetLysThrGluSerLeu 668

Db       2464 --------------GCTAGCTACGGGTTTGGGAATCAGCATATGAAAACCTCATAT--- 2505

Qy        669 ProProProProProThrLeuSerThrAsp---HisThrSerTrpGlyGlyTyrValTrp 687

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Qy        688 AlaGlyGluLeuGlyThrArgValAlaValGluAsnThrSerGlyArgGlyPhePheGln 707

Db       2551 GCTGGAGAGATTGGAGCGGGATTACCGATTGTGATTACTCCATCTAAGCTCTATTTGAAT 2610

Qy        708 GluTyrThrProPheValLysValGlnAlaValTyrAlaArgGlnAspSerPheValGlu 727

Db       2611 GAGTTGCGTCCTTTCGTGCAAGCTGAGTTTTCTTATGCCGATCATGAATCTTTTACAGAG 2670

Qy        728 LeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyrAsnLeuAlaIleProLeu 747

Db       2671 GAAGGCGATCAAGCTCGGGCATTCAAGAGCGGACATCTCCTAAATCTATCAGTTCCTGTT 2730

Qy        748 GlyIleLysLeuGluLysArgPheAla------GluGlnTyrTyrHisValValAlaMet 765

Db       2731 GGAGTGAAGTTTGATCGATGTTCTAGTACACATCCTAATAAATATAGCTTTATGGCGGCT 2790

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Qy        786 GlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSer 805

Db       2851 GAGACATGGACAACAGATGCCTTTCATTTAGCAAGACATGGAGTTGTGGTTAGAGGATCT 2910

Qy        806 GlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTrpArg 825

Db       2911 ATGTATGCTTCTCTAACAAGTAATATAGAAGTATATGGCCATGGAAGATATGAGTATCGA 2970

Qy        826 GlySerSerArgSerTyrAsnValAspAlaGlySerLysIleLysPhe 841

Db       2971 GATGCTTCTCGAGGCTATGGTTTGAGTGCAGGAAGTAAAGTCCGGTTC 3018
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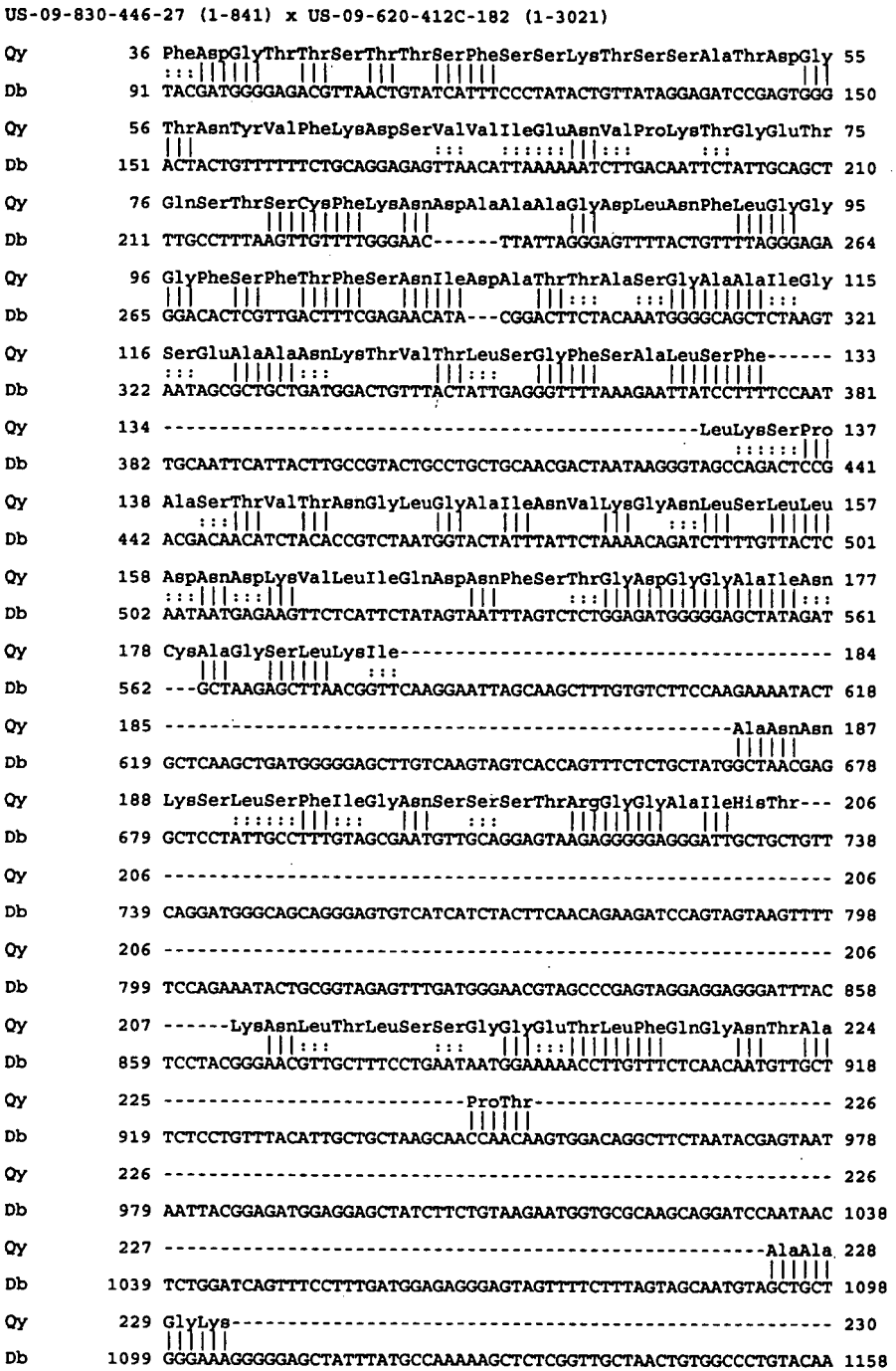
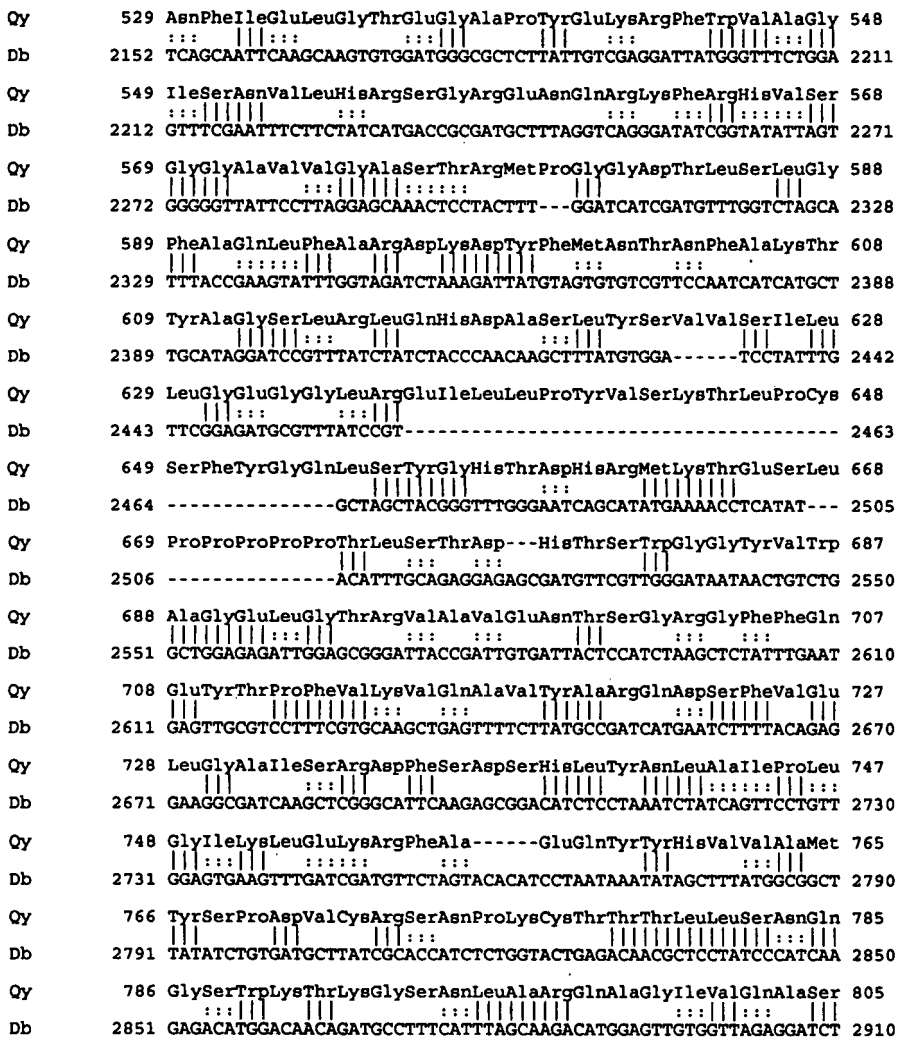
RESULT 4
US-09-620-412C-182
; Sequence 182, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 182
; LENGTH: 3021
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-182

Alignment Scores:

Pred. No.:	5.22e-91	Length:	3021
Score:	939.00	Matches:	285
Percent Similarity:	39.77%	Conservative:	127
Best Local Similarity:	27.51%	Mismatches:	334
Query Match:	21.86%	Indels:	290
DB:	4	Gaps:	29

US-09-830-446-27 (1-841) x US-09-620-412C-182 (1-3021)



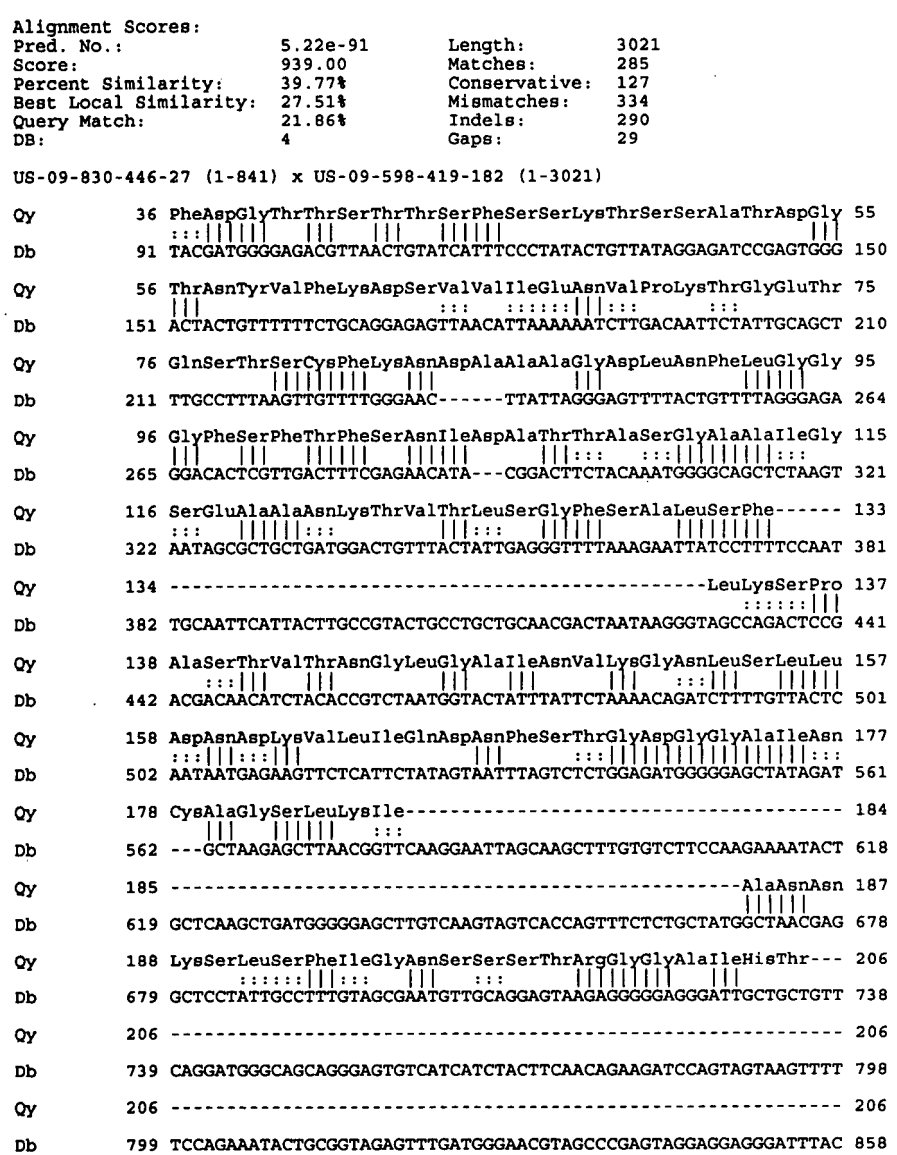


RESULT 5
US-09-598-419-182
; Sequence 182, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 182
; LENGTH: 3021
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-598-419-182

Alignment Scores:

Pred. No.:	5.22e-91	Length:	3021
Score:	939.00	Matches:	285
Percent Similarity:	39.77%	Conservative:	127
Best Local Similarity:	27.51%	Mismatches:	334
Query Match:	21.86%	Indels:	290
DB:	4	Gaps:	29

US-09-830-446-27 (1-841) x US-09-598-419-182 (1-3021)

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Qy 226 ---------- 226
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Qy 227 ----------AlaAla 228
Db 1039 TCTGGATCAGTTTCCTTTGATGGAGAGGGAGTAGTTTTCTTTAGTAGCAATGTAGCTGCT 1098
Qy 229 GlyLys---------- 230
Db 1099 GGGAAAGGGGGAGCTATTTATGCCAAAAAGCTCTCGGTTGCTAACTGTGGCCCTGTACAA 1158
Qy 231 ----------GlyGlyAlaIleAlaIleAlaAspSerGlyThrLeu 242
Db 1159 TTTTTAAGGAATATCGCTAATGATGGTGGAGCGATTTATTTAGGAGAATCTGGAGAGCTC 1218
Qy 243 SerIleSerGlyAspSerGlyAspIleIlePheGluGly---------- 255
Db 1219 AGTTTATCTGCTGATTATGGAGATATTATTTTCGATGGGAATCTTAAAAGAACAGCCAAA 1278
Qy 256 ---AsnThrIleGlyAlaThrGly---ThrValSerHisSerAlaIleAspLeuGlyThr 273
Db 1279 GAGAATGCTGCCGATGTTAATGGCGTAACTGTGTCCTCACAAGCCATTTCGATGGGATCG 1338
Qy 274 SerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspPro 293
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Qy 330 LeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSerLysLeuLeuGlnAsnVal 349
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Qy 350 AlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsnGlyPhe 369
Db 1525 ACGATAGAGCAAGGAAGGATTGTTCTTCGTGAAAAGGCAAAATTATCAGTGAATTCTCTA 1584
Qy 370 SerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeu---------- 385
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Db 1762 GCGCAAGATTCTCATCCTGCAGTCATTGGTAGCACAACTGCTGGTTCTGTTACAATTAGT 1821
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Qy 445 AspHisSerTyrAsp----------GlyIleLeuGluLeuAspAla 456
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Qy 457 GlyLysAspIleValIleSerAlaAspSerArgSerIleAspAlaValGlnSerPro--- 475
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Qy 476 TyrGlyTyrGlnGlyLysTrpThrIleAsnTrpSerThrAspAspLys---------- 491
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Db 2038 TATACTCTGAAAGCTACA------TGGACTAAAACTGGGTATAATCCTGGGCCTGAGCGA 2091
Qy 509 GluAlaProLeuValProAsnLeuLeuTrpGlySerPheIleAspValArgSerPheGln 528
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Qy 529 AsnPheIleGluLeuGlyThrGluGlyAlaProTyrGluLysArgPheTrpValAlaGly 548
Db 2152 TCAGCAATTCAAGCAAGTGTGGATGGGCGCTCTTATTGTCGAGGATTATGGGTTTCTGGA 2211
Qy 549 IleSerAsnValLeuHisArgSerGlyArgGluAsnGlnArgLysPheArgHisValSer 568
Db 2212 GTTTCGAATTTCTTCTATCATGACCGCGATGCTTTAGGTCAGGGATATCGGTATATTAGT 2271
Qy 569 GlyGlyAlaValValGlyAlaSerThrArgMetProGlyGlyAspThrLeuSerLeuGly 588
Db 2272 GGGGGTTATTCCTTAGGAGCAAACTCCTACTTT---GGATCATCGATGTTTGGTCTAGCA 2328
Qy 589 PheAlaGlnLeuPheAlaArgAspLysAspTyrPheMetAsnThrAsnPheAlaLysThr 608
Db 2329 TTTACCGAAGTATTTGGTAGATCTAAAGATTATGTAGTGTGTCGTTCCAATCATCATGCT 2388
Qy 609 TyrAlaGlySerLeuArgLeuGlnHisAspAlaSerLeuTyrSerValValSerIleLeu 628
Db 2389 TGCATAGGATCCGTTTATCTATCTACCCAACAAGCTTTATGTGGA------TCCTATTTG 2442
Qy 629 LeuGlyGluGlyGlyLeuArgGluIleLeuLeuProTyrValSerLysThrLeuProCys 648
Db 2443 TTCGGAGATGCGTTTATCCGT---------- 2463
Qy 649 SerPheTyrGlyGlnLeuSerTyrGlyHisThrAspHisArgMetLysThrGluSerLeu 668
Db 2464 --------------GCTAGCTACGGGTTTGGGAATCAGCATATGAAAACCTCATAT--- 2505
Qy 669 ProProProProProThrLeuSerThrAsp---HisThrSerTrpGlyGlyTyrValTrp 687
Db 2506 --------------ACATTTGCAGAGGAGAGCGATGTTCGTTGGGATAATAACTGTCTG 2550
Qy 688 AlaGlyGluLeuGlyThrArgValAlaValGluAsnThrSerGlyArgGlyPhePheGln 707
Db 2551 GCTGGAGAGATTGGAGCGGGATTACCGATTGTGATTACTCCATCTAAGCTCTATTTGAAT 2610
Qy 708 GluTyrThrProPheValLysValGlnAlaValTyrAlaArgGlnAspSerPheValGlu 727
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Qy 728 LeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyrAsnLeuAlaIleProLeu 747
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Qy 748 GlyIleLysLeuGluLysArgPheAla------GluGlnTyrTyrHisValValAlaMet 765
Db 2731 GGAGTGAAGTTTGATCGATGTTCTAGTACACATCCTAATAAATATAGCTTTATGGCGGCT 2790
Qy 766 TyrSerProAspValCysArgSerAsnProLysCysThrThrThrLeuLeuSerAsnGln 785
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Db       2971 GATGCTTCTCGAGGCTATGGTTTGAGTGCAGGAAGTAAAGTCCGGTTC 3018
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RESULT 6
US-09-556-877-170
; Sequence 170, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 170
; LENGTH: 2949
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-556-877-170

Alignment Scores:

Pred. No.:	1.06e-90	Length:	2949
Score:	936.00	Matches:	285
Percent Similarity:	39.67%	Conservative:	126
Best Local Similarity:	27.51%	Mismatches:	335
Query Match:	21.79%	Indels:	290
DB:	4	Gaps:	29

US-09-830-446-27 (1-841) x US-09-556-877-170 (1-2949)

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Db         79 ACTACTGTTTTTTCTGCAGGAGAGTTAACATTAAAAAATCTTGACAATTCTATTGCAGCT 138

Qy         76 GlnSerThrSerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGly 95

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Qy        134 ----------------------------------------------LeuLysSerPro 137

Db        310 TGCAATTCATTACTTGCCGTACTGCCTGCTGCAACGACTAATAAGGGTAGCCAGACTCCG 369

Qy        138 AlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeu 157

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Qy        231 ------------------------GlyGlyAlaIleAlaIleAlaAspSerGlyThrLeu 242

Db       1087 TTTTTAAGGAATATCGCTAATGATGGTGGAGCGATTTATTTAGGAGAATCTGGAGAGCTC 1146

Qy        243 SerIleSerGlyAspSerGlyAspIleIlePheGluGly--------------------- 255

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Qy        256 ---AsnThrIleGlyAlaThrGly---ThrValSerHisSerAlaIleAspLeuGlyThr 273

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Qy        386 --------------------ValAlaAsnThrGluSerIleGluLeuThrAsnLeuGlu 398
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Qy        411 ------------------LysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAsp 424
Db       1690 GCGCAAGATTCTCATCCTGCAGTCATTGGTAGCACAACTGCTGGTTCTGTTACAATTAGT 1749

Qy        425 ArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeuAsnGlu 444
Db       1750 GGGCCTATCTTTTTTGAGGATTTGGATGATACAGCTTATGATAGG-------------- 1794

Qy        445 AspHisSerTyrAsp-----------------------GlyIleLeuGluLeuAspAla 456
Db       1795 ---------TATGATTGGCTAGGTTCTAATCAAAAAATCAATGTCCTGAAATTACAGTTA 1845

Qy        457 GlyLysAspIleValIleSerAlaAspSerArgSerIleAspAlaValGlnSerPro--- 475
Db       1846 GGGACTAAGCCCCCAGCTAATGCCCCATCAGATTTGACTCTAGGGAATGAGATGCCTAAG 1905

Qy        476 TyrGlyTyrGlnGlyLysTrpThrIleAsnTrpSerThrAspAspLys---------- 491
Db       1906 TATGGCTATCAAGGAAGCTGGAAGCTTGCGTGGGATCCTAATACAGCAAATAATGGTCCT 1965

Qy        492 ---------LysAlaThrValSerTrpAlaLysGlnSerPheAsnProThrAlaGluGln 508
Db       1966 TATACTCTGAAAGCTACA------TGGACTAAAACTGGGTATAATCCTGGGCCTGAGCGA 2019

Qy        509 GluAlaProLeuValProAsnLeuLeuTrpGlySerPheIleAspValArgSerPheGln 528
Db       2020 GTAGCTTCTTTGGTTCCAAATAGTTTATGGGGATCCATTTTAGATATACGATCTGCGCAT 2079

Qy        529 AsnPheIleGluLeuGlyThrGluGlyAlaProTyrGluLysArgPheTrpValAlaGly 548
Db       2080 TCAGCAATTCAAGCAAGTGTGGATGGGCGCTCTTATTGTCGAGGATTATGGGTTTCTGGA 2139

Qy        549 IleSerAsnValLeuHisArgSerGlyArgGluAsnGlnArgLysPheArgHisValSer 568
Db       2140 GTTTCGAATTTCTTCTATCATGACCGCGATGCTTTAGGTCAGGGATATCGGTATATTAGT 2199

Qy        569 GlyGlyAlaValValGlyAlaSerThrArgMetProGlyGlyAspThrLeuSerLeuGly 588
Db       2200 GGGGGTTATTCCTTAGGAGCAAACTCCTACTTT---GGATCATCGATGTTTGGTCTAGCA 2256

Qy        589 PheAlaGlnLeuPheAlaArgAspLysAspTyrPheMetAsnThrAsnPheAlaLysThr 608
Db       2257 TTTACCGAAGTATTTGGTAGATCTAAAGATTATGTAGTGTGTCGTTCCAATCATCATGCT 2316

Qy        609 TyrAlaGlySerLeuArgLeuGlnHisAspAlaSerLeuTyrSerValValSerIleLeu 628
Db       2317 TGCATAGGATCCGTTTATCTATCTACCCAACAAGCTTTATGTGGA------TCCTATTTG 2370

Qy        629 LeuGlyGluGlyGlyLeuArgGluIleLeuLeuProTyrValSerLysThrLeuProCys 648
Db       2371 TTCGGAGATGCGTTTATCCGT----------------------------------- 2391

Qy        649 SerPheTyrGlyGlnLeuSerTyrGlyHisThrAspHisArgMetLysThrGluSerLeu 668
Db       2392 ---------------GCTAGCTACGGGTTTGGGAATCAGCATATGAAAACCTCATAT--- 2433

Qy        669 ProProProProProThrLeuSerThrAsp---HisThrSerTrpGlyGlyTyrValTrp 687
Db       2434 ---------------ACATTTGCAGAGGAGAGCGATGTTCGTTGGGATAATAACTGTCTG 2478

Qy        688 AlaGlyGluLeuGlyThrArgValAlaValGluAsnThrSerGlyArgGlyPhePheGln 707
Db       2479 GCTGGAGAGATTGGAGCGGGATTACCGATTGTGATTACTCCATCTAAGCTCTATTTGAAT 2538

Qy        708 GluTyrThrProPheValLysValGlnAlaValTyrAlaArgGlnAspSerPheValGlu 727
Db       2539 GAGTTGCGTCCTTTCGTGCAAGCTGAGTTTTCTTATGCCGATCATGAATCTTTTACAGAG 2598

Qy        728 LeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyrAsnLeuAlaIleProLeu 747
Db       2599 GAAGGCGATCAAGCTCGGGCATTCAAGAGCGGACATCTCCTAAATCTATCAGTTCCTGTT 2658

Qy        748 GlyIleLysLeuGluLysArgPheAla------GluGlnTyrTyrHisValValAlaMet 765
Db       2659 GGAGTGAAGTTTGATCGATGTTCTAGTACACATCCTAATAAATATAGCTTTATGGCGGCT 2718

Qy        766 TyrSerProAspValCysArgSerAsnProLysCysThrThrThrLeuLeuSerAsnGln 785
Db       2719 TATATCTGTGATGCTTATCGCACCATCTCTGGTACTGAGACAACGCTCCTATCCCATCAA 2778

Qy        786 GlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSer 805
Db       2779 GAGACATGGACAACAGATGCCTTTCATTTAGCAAGACATGGAGTTGTGGTTAGAGGATCT 2838

Qy        806 GlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTrpArg 825
Db       2839 ATGTATGCTTCTCTAACAAGTAATATAGAAGTATATGGCCATGGAAGATATGAGTATCGA 2898

Qy        826 GlySerSerArgSerTyrAsnValAspAlaGlySerLysIleLysPhe 841
Db       2899 GATGCTTCTCGAGGCTATGGTTTGAGTGCAGGMAGTAAAGTCYGGTTC 2946

RESULT 7
US-09-620-412C-170
; Sequence 170, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
;  APPLICANT: Steven P. Fling
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
;  TITLE OF INVENTION:  DIAGNOSIS OF CHLAMYDIAL INFECTION
;  FILE REFERENCE: 210121.469C7
;  CURRENT APPLICATION NUMBER: US/09/620,412C
;  CURRENT FILING DATE:  2000-07-20
;  NUMBER OF SEQ ID NOS: 363
;  SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 170
;   LENGTH: 2949
;   TYPE: DNA
;   ORGANISM: Chlamydia
US-09-620-412C-170

Alignment Scores:
Pred. No.:                1.06e-90        Length:          2949
Score:                    936.00          Matches:         285
Percent Similarity:       39.67%          Conservative:    126
Best Local Similarity:    27.51%          Mismatches:      335
Query Match:              21.79%          Indels:          290
DB:                       4               Gaps:            29

US-09-830-446-27 (1-841) x US-09-620-412C-170 (1-2949)

Qy         36 PheAspGlyThrThrSerThrThrSerPheSerSerLysThrSerSerAlaThrAspGly 55
Db         19 TACGATGGGGAGACGTTAACTGTATCATTTCCCTATACTGTTATAGGAGATCCGAGTGGG 78

Qy         56 ThrAsnTyrValPheLysAspSerValValIleGluAsnValProLysThrGlyGluThr 75
Db         79 ACTACTGTTTTTTCTGCAGGAGAGTTAACATTAAAAAATCTTGACAATTCTATTGCAGCT 138

Qy         76 GlnSerThrSerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGly 95
Db        139 TTGCCTTTAAGTTGTTTTGGGAAC------TTATTAGGGAGTTTTACTGTTTTAGGGAGA 192
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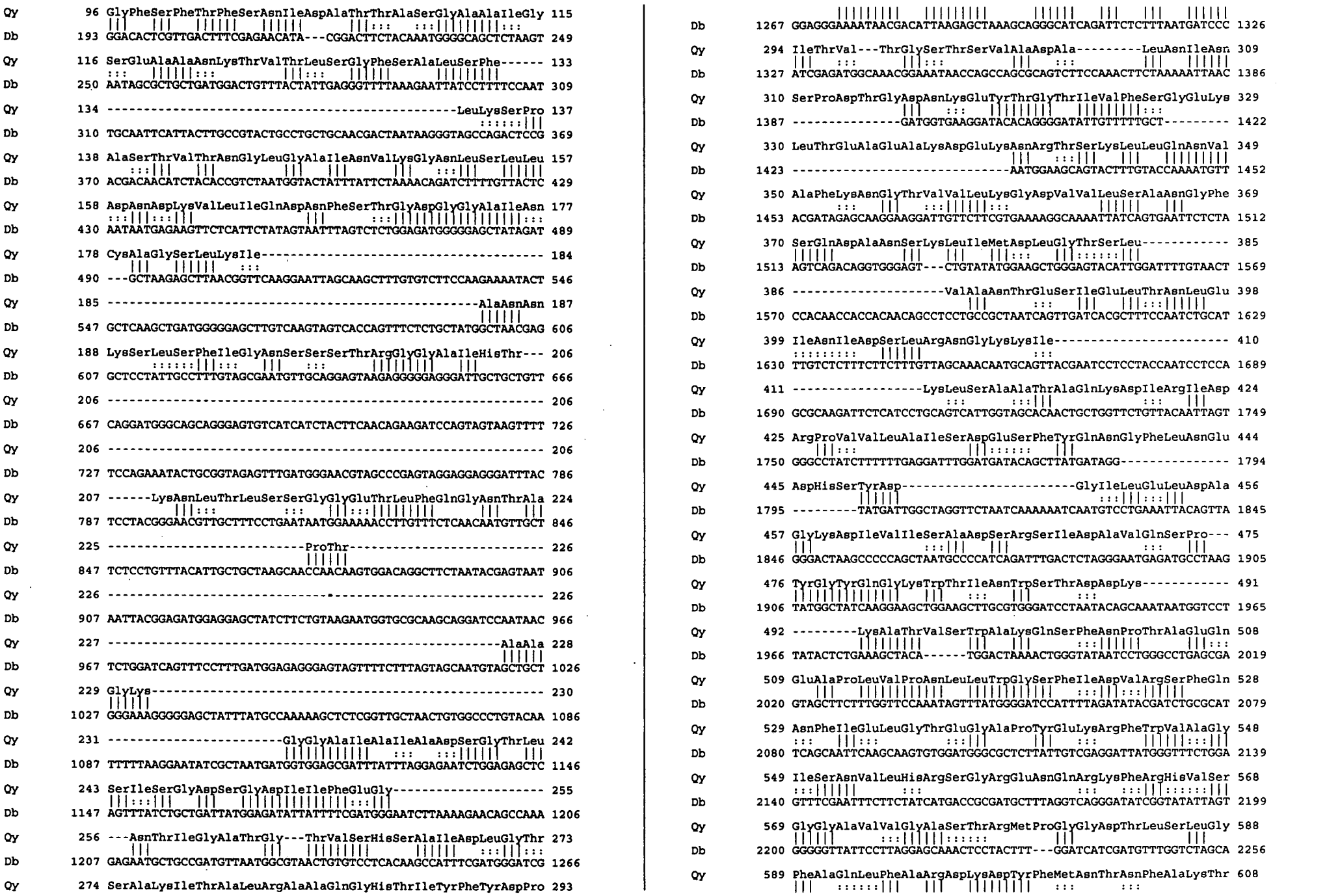

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Db       2257 TTTACCGAAGTATTTGGTAGATCTAAAGATTATGTAGTGTGTCGTTCCAATCATCATGCT 2316

Qy        609 TyrAlaGlySerLeuArgLeuGlnHisAspAlaSerLeuTyrSerValValSerIleLeu 628

Db       2317 TGCATAGGATCCGTTTATCTATCTACCCAACAAGCTTTATGTGGA------TCCTATTTG 2370

Qy        629 LeuGlyGluGlyGlyLeuArgGluIleLeuLeuProTyrValSerLysThrLeuProCys 648

Db       2371 TTCGGAGATGCGTTTATCCGT----------------------------------------- 2391

Qy        649 SerPheTyrGlyGlnLeuSerTyrGlyHisThrAspHisArgMetLysThrGluSerLeu 668

Db       2392 --------------GCTAGCTACGGGTTTGGGAATCAGCATATGAAAACCTCATAT--- 2433

Qy        669 ProProProProProThrLeuSerThrAsp---HisThrSerTrpGlyGlyTyrValTrp 687

Db       2434 --------------ACATTTGCAGAGGAGAGCGATGTTCGTTGGGATAATAACTGTCTG 2478

Qy        688 AlaGlyGluLeuGlyThrArgValAlaValGluAsnThrSerGlyArgGlyPhePheGln 707

Db       2479 GCTGGAGAGATTGGAGCGGGATTACCGATTGTGATTACTCCATCTAAGCTCTATTTGAAT 2538

Qy        708 GluTyrThrProPheValLysValGlnAlaValTyrAlaArgGlnAspSerPheValGlu 727

Db       2539 GAGTTGCGTCCTTTCGTGCAAGCTGAGTTTTCTTATGCCGATCATGAATCTTTTACAGAG 2598

Qy        728 LeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyrAsnLeuAlaIleProLeu 747

Db       2599 GAAGGCGATCAAGCTCGGGCATTCAAGAGCGGACATCTCCTAAATCTATCAGTTCCTGTT 2658

Qy        748 GlyIleLysLeuGluLysArgPheAla------GluGlnTyrTyrHisValValAlaMet 765

Db       2659 GGAGTGAAGTTTGATCGATGTTCTAGTACACATCCTAATAAATATAGCTTTATGGCGGCT 2718

Qy        766 TyrSerProAspValCysArgSerAsnProLysCysThrThrThrLeuLeuSerAsnGln 785

Db       2719 TATATCTGTGATGCTTATCGCACCATCTCTGGTACTGAGACAACGCTCCTATCCCATCAA 2778

Qy        786 GlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSer 805

Db       2779 GAGACATGGACAACAGATGCCTTTCATTTAGCAAGACATGGAGTTGTGGTTAGAGGATCT 2838

Qy        806 GlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTrpArg 825

Db       2839 ATGTATGCTTCTCTAACAAGTAATATAGAAGTATATGGCCATGGAAGATATGAGTATCGA 2898

Qy        826 GlySerSerArgSerTyrAsnValAspAlaGlySerLysIleLysPhe 841

Db       2899 GATGCTTCTCGAGGCTATGGTTTGAGTGCAGGMAGTAAAGTCYGGTTC 2946
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RESULT 8
US-09-598-419-170
; Sequence 170, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 170
; LENGTH: 2949
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-598-419-170

Alignment Scores:

Pred. No.:	1.06e-90	Length:	2949
Score:	936.00	Matches:	285

Percent Similarity:	39.67%	Conservative:	126
Best Local Similarity:	27.51%	Mismatches:	335
Query Match:	21.79%	Indels:	290
DB:	4	Gaps:	29

US-09-830-446-27 (1-841) x US-09-598-419-170 (1-2949)

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Qy         36 PheAspGlyThrThrSerThrThrSerPheSerSerLysThrSerSerAlaThrAspGly 55

Db         19 TACGATGGGGAGACGTTAACTGTATCATTTCCCTATACTGTTATAGGAGATCCGAGTGGG 78

Qy         56 ThrAsnTyrValPheLysAspSerValValIleGluAsnValProLysThrGlyGluThr 75

Db         79 ACTACTGTTTTTTCTGCAGGAGAGTTAACATTAAAAAATCTTGACAATTCTATTGCAGCT 138

Qy         76 GlnSerThrSerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGly 95

Db        139 TTGCCTTTAAGTTGTTTTGGGAAC------TTATTAGGGAGTTTTACTGTTTTAGGGAGA 192

Qy         96 GlyPheSerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGly 115

Db        193 GGACACTCGTTGACTTTCGAGAACATA---CGGACTTCTACAAATGGGGCAGCTCTAAGT 249

Qy        116 SerGluAlaAlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPhe------ 133

Db        250 AATAGCGCTGCTGATGGACTGTTTACTATTGAGGGTTTTAAAGAATTATCCTTTTCCAAT 309

Qy        134 ----------------------------------------------LeuLysSerPro 137

Db        310 TGCAATTCATTACTTGCCGTACTGCCTGCTGCAACGACTAATAAGGGTAGCCAGACTCCG 369

Qy        138 AlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeu 157

Db        370 ACGACAACATCTACACCGTCTAATGGTACTATTTATTCTAAAACAGATCTTTTGTTACTC 429

Qy        158 AspAsnAspLysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsn 177

Db        430 AATAATGAGAAGTTCTCATTCTATAGTAATTTAGTCTCTGGAGATGGGGGAGCTATAGAT 489

Qy        178 CysAlaGlySerLeuLysIle---------------------------------------- 184

Db        490 ---GCTAAGAGCTTAACGGTTCAAGGAATTAGCAAGCTTTGTGTCTTCCAAGAAAATACT 546

Qy        185 ----------------------------------------------AlaAsnAsn 187

Db        547 GCTCAAGCTGATGGGGGAGCTTGTCAAGTAGTCACCAGTTTCTCTGCTATGGCTAACGAG 606

Qy        188 LysSerLeuSerPheIleGlyAsnSerSerSerThrArgGlyGlyAlaIleHisThr--- 206

Db        607 GCTCCTATTGCCTTTGTAGCGAATGTTGCAGGAGTAAGAGGGGGAGGGATTGCTGCTGTT 666

Qy        206 ------------------------------------------------------------ 206

Db        667 CAGGATGGGCAGCAGGGAGTGTCATCATCTACTTCAACAGAAGATCCAGTAGTAAGTTTT 726

Qy        206 ------------------------------------------------------------ 206

Db        727 TCCAGAAATACTGCGGTAGAGTTTGATGGGAACGTAGCCCGAGTAGGAGGAGGGATTTAC 786

Qy        207 ------LysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAla 224

Db        787 TCCTACGGGAACGTTGCTTTCCTGAATAATGGAAAAACCTTGTTTCTCAACAATGTTGCT 846

Qy        225 ----------------------------ProThr---------------------------- 226

Db        847 TCTCCTGTTTACATTGCTGCTAAGCAACCAACAAGTGGACAGGCTTCTAATACGAGTAAT 906

Qy        226 ------------------------------------------------------------ 226

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Qy        227 ----------------------------------------------------AlaAla 228
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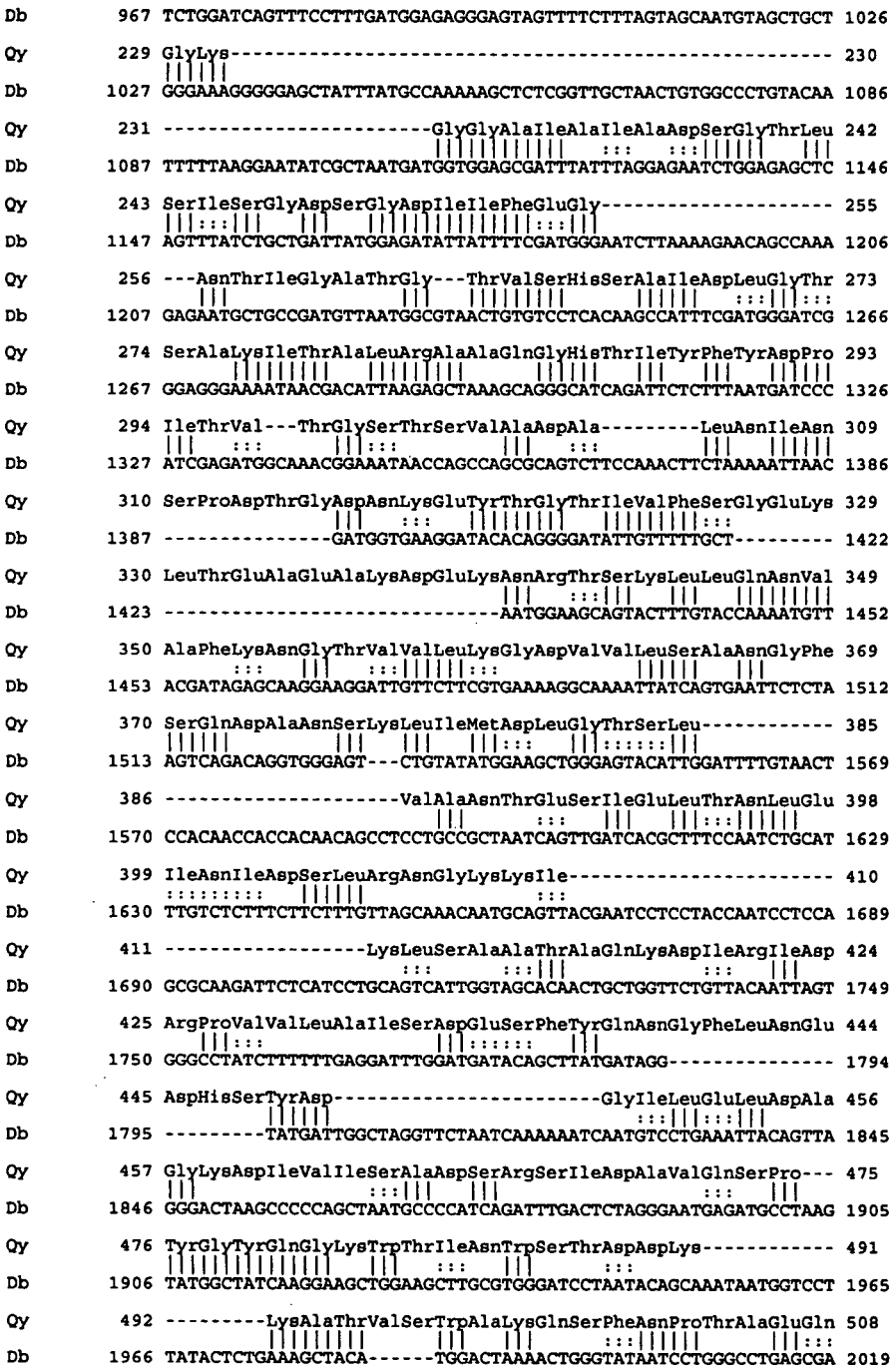

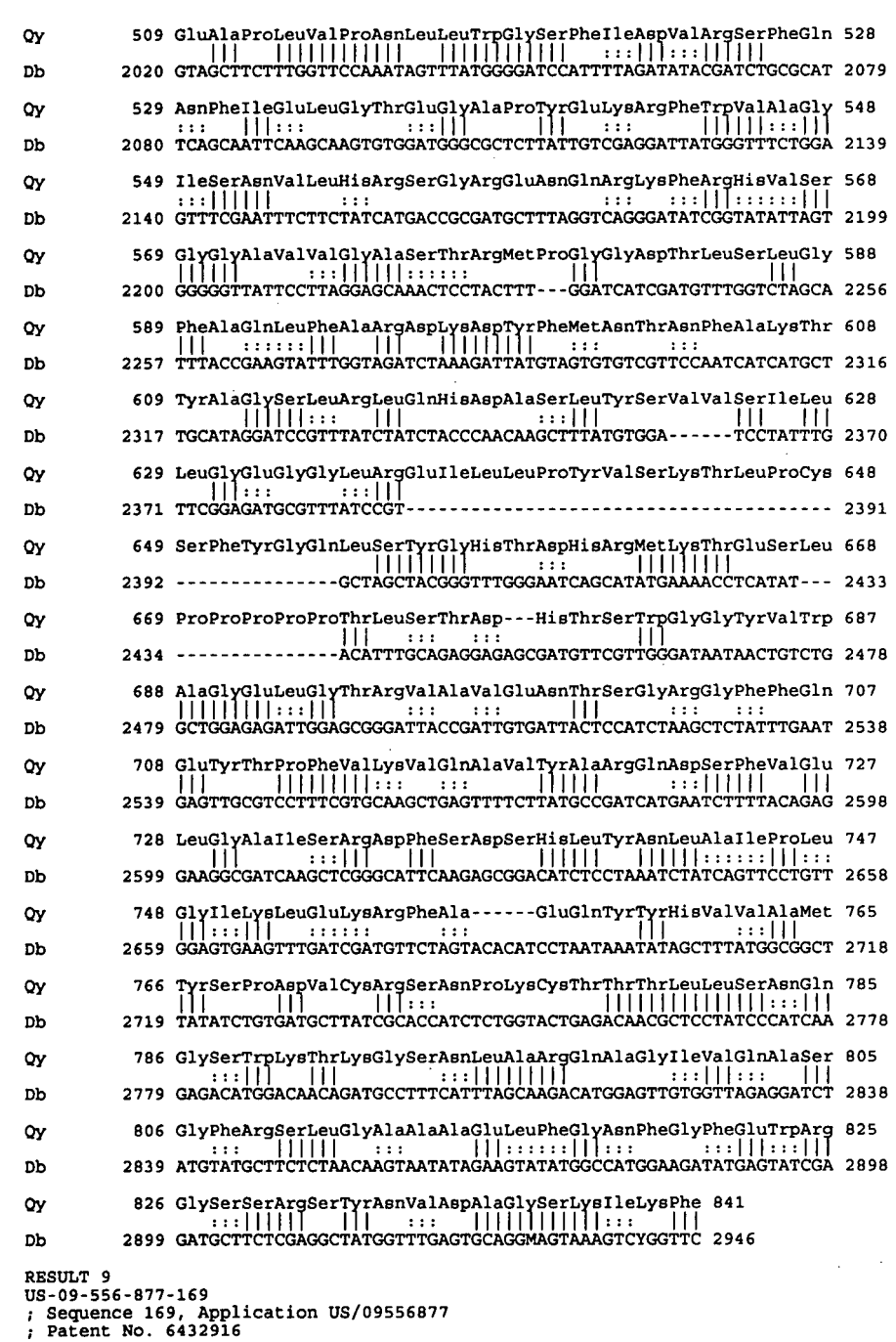

RESULT 9
US-09-556-877-169
; Sequence 169, Application US/09556877
; Patent No. 6432916

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; GENERAL INFORMATION:
;  APPLICANT:  Probst, Peter
;  APPLICANT:  Bhatia, Ajay
;  APPLICANT:  Skeiky, Yasir
;  APPLICANT:  Fling, Steve
;  APPLICANT:  Maisonneuve, Jeff
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR TREATMENT AND
;  TITLE OF INVENTION:  DIAGNOSIS OF CHLAMYDIAL INFECTION
;  FILE REFERENCE:  210121.469C5
;  CURRENT APPLICATION NUMBER: US/09/556,877
;  CURRENT FILING DATE:  2000-04-19
;  NUMBER OF SEQ ID NOS:  305
;  SOFTWARE:  FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 169
;   LENGTH: 2643
;   TYPE: DNA
;   ORGANISM: Chlamydia
US-09-556-877-169

Alignment Scores:
Pred. No.:                1.76e-66      Length:          2643
Score:                    711.50        Matches:         241
Percent Similarity:       44.75%        Conservative:    138
Best Local Similarity:    28.45%        Mismatches:      347
Query Match:              16.57%        Indels:          121
DB:                       4             Gaps:            31

US-09-830-446-27 (1-841) x US-09-556-877-169 (1-2643)

Qy         41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
              |||   |||      |||||||||   ||||||
Db        325 TCCTTCACAGATTGCTCTTCCAAGGAAAGCTCT-------------------------- 357

Qy         61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGln------------ 76
                  |||::::::   :::         |||   |||:::
Db        358 ---CCTTCTATTATTCATCAA---------AAGAATGGTCAGTTATCCTTGCGCAATAAT 405

Qy         77 ---SerThrSerCysPheLysAsn----------------AspAlaAlaAlaGlyAsp 89
                 |||   |||      :::|||                |||  :::  |||
Db        406 GGTAGCATGAGTTTCTGTCGAAATCATGCTGAAGGCTCTGGAGGAGCCATCTCTGCGGAT 465

Qy         90 LeuAsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThrAla 109
                  |||         :::   ||||||          :::::::::
Db        466 GCCTTTTCTCTACAGCACAACTATCTTTTCACAGCTTTTGAAGAGAATTCTTCTAAAGGA 525

Qy        110 SerGlyAlaAlaIleGlySerGluAlaAlaAsnLysThrValThrLeuSer---GlyPhe 128
              :::|||   ||||||   ::::::          |||   :::||||||
Db        526 AATGGCGGAGCCATTCAGGCTCAA-----------ACCTTCTCTTTATCTAGAAATGTG 573

Qy        129 SerAlaLeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIle 148
              |||   :::||||||   ::::::   |||          ||||||   |||||||||
Db        574 TCGCCTATTTCTTTCGCCCGTAATCGTGCGGAT------TTAAATGGC---GGCGCTATT 624

Qy        149 AsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsnPhe 168
                  ||||||            |||         |||
Db        625 ---TGCTGTAGTAATCTTATTTGTTCAGGGAATGTAAACCCTCTCTTTTTCACTGGAAAC 681

Qy        169 SerThrGlyAspGlyGlyAlaIleAsnCys----------------------AlaGly 180
              |||      :::||||||||||||   |||                       |||
Db        682 TCCGCCACGAATGGAGGCGCTATTTGTTGTATCAGCGATCTAAACACCTCAGAAAAAGGC 741

Qy        181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArg 200
              ||||||   :::|||   |||:::         |||      ||||||:::      :::
Db        742 TCTCTCTCTCTTGCTTGTAACCAAGAAACGCTATTTGCAAGCAATTCTGCTAAAGAAAAA 801

Qy        201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220
              ||||||||||||:::   |||::::::   |||          |||          |||
Db        802 GGCGGGGCTATTTATGCCAAGCACATGGTATTGCGTTATAACGGTCCTGTTTCCTTCATT 861

Qy        221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240
                 |||:::|||                |||||||||||||||||              |||
Db        862 AACAACAGCGCTAAAATA-----------GGTGGAGCTATCGCCATCCAGTCCGGAGGG 909

Qy        241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThr------Ile 258
              :::|||||||||           |||   ::::::|||:::   |||:::
Db        910 AGTCTCTCTATCCTTGCAGGTGAAGGATCTGTTCTGTTCCAGAATAACTCCCAACGCACC 969

Qy        259 GlyAlaThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThr 278
                     |||   |||      :::||||||   |||          |||   ::::::
Db        970 TCCGACCAAGGTCTAGTA---AGAAACGCCATCTACTTARAGAAAGATGCGATTCTTTCT 1026

Qy        279 AlaLeuArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGly 298
              :::|||   |||      |||      |||   |||:::|||||||||   |||
Db       1027 TCCTTAGAAGCTCGCAACGGA---GATATTCTTTTCTTTGATCCTATT---GTACAAGAA 1080

Qy        299 SerThrSerValAlaAspAlaLeu-----------------AsnIleAsnSerPro--- 311
              |||:::|||           |||                 ::::::   ||||||
Db       1081 AGTAGCAGCAAAGAATCGCCTCTTCCCTCCTCTTTGCAAGCCAGCGTGACTTCTCCCACC 1140

Qy        312 -------------------------AspThrGlyAspAsnLysGluTyrThrGlyThr 322
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Db       1141 CCAGCCACCGCATCTCCTTTAGTTATTCAGACAAGTGCAAACCGT------------TCA 1188

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Db       1246 TCCCAACTACAGCAGCCTATCGAACTGAAATCCGGACGCTTAGTTTTAAAAGATCGCGCT 1305

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Db       1306 GTCCTTTCCGCGCCTTCTCTCTCTCAGGATCCTCAAGCTCTCCTCATTATGGAAGCGGGA 1365

Qy        383 ThrSerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAsp 402
              |||||||||       :::::::::   ::::::|||       |||   |||   :::
Db       1366 ACTTCTTTAAAAACTTCCTCTGAT---TTGAAGTTAGCTACGCTAAGTATTCCCCTTCAT 1422

Qy        403 SerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArg 422
              ||||||          |||   :::   :::   |||                ::::::
Db       1423 TCCTTAGATACTGAAAAAAGCGTAACTATCCACGCC------------CCTAATCTTTCT 1470

Qy        423 IleAspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsn---GlyPhe 441
              |||   :::      :::              |||||:::||||||:::|||
Db       1471 ATCCAAAAGATCTTCCTCTCTAACTCTGGAGATGAGAATTTTTATGAAAATGTAGAGCTT 1530

Qy        442 LeuAsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleVal 461
              |||:::::::::   :::         :::|||   |||          :::      :::
Db       1531 CTCAGTAAAGAGCAAAACAATATTCCTCTCCTTACTCTCCCTAAAGAGCAATCTCATTTA 1590

Qy        462 IleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGlyLys 481
                        |||                 :::   |||   :::||||||||||||
Db       1591 CATCTTCCTGATGGGAAC-----------CTCTCTTCTCACTTTGGATATCAAGGAGAT 1638

Qy        482 TrpThrIleAsnTrpSerThrAspAspLys------LysAlaThrValSerTrpAlaLys 499
              ||||||   :::|||          |||:::                 :::|||
Db       1639 TGGACTTTTCTTGGAAAGATTCTGATGAAGGGCATTCTCTGATTGCTAATTGGACGCCT 1698

Qy        500 GlnSerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGly 519
              :::::::::   |||       |||:::::::::   ||||||   |||   ||||||
Db       1699 AAAAACTATGTGCCTCATCCAGAACGTCAATCTACACTCGTTGCGAACACTCTTTGGAAC 1758

Qy        520 SerPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaPro 539
              ::::::   |||:::::::::   |||:::   |||                |||
Db       1759 ACCTATTCCGATATGCAAGCTGTGCAGTCGATGATTAATACAACAGCGCACGGAGGAGCC 1818

Qy        540 TyrGluLysArgPheTrpValAlaGlyIleSerAsnVal------LeuHisArgSerGly 557
              |||                |||   :::   :::||||||:::      :::|||   |||
Db       1819 TATCTATTTGGAACGTGGGGATCTGCTGTTTCTAATTTATTCTATGTTCACGACAGCTCT 1878

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Db       1879 GGGAAACCTATCGATAATTGGCATCATAGAAGCCTTGGCTACCTATTCGGTATCAGTACT 1938

Qy        578 ArgMetProGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLys 597
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Db       1939 CACAGTTTAGATGACCATTCTTTCTGCTTGGCTGCAGGACAATTACTCGGGAAATCGTCC 1998

Qy        598 AspTyrPheMetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHis 617

Db       1999 GATTCCTTTATTACGTCTACAGAAACGACCTCCTATATAGCTACTGTACAAGCGCAACTC 2058

Qy        618 AspAlaSerLeuTyrSerValValSerIleLeuGlyGluGlyGlyLeuArgGluIle 637

Db       2059 GCTACCTCTCTAATGAAAATCTCTGCA------------------------------- 2085

Qy        638 LeuLeuProTyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGly 657

Db       2086 ----------------------------------------CAGGCATGCTACAAT 2100

Qy        658 HisThrAspHisArgMetLysThrGluSerLeuProProProProProThrLeuSerThr 677

Db       2101 GAAAGTATCCATGAGCTAAAAACAAAATAT--------------CGCTCCTTCTCTAAA 2145

Qy        678 Asp---HisThrSerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAla 696

Db       2146 GAAGGATTCGGATCCTGGCATAGCGTTGCAGTATCCGGAGAAGTGTGCGCATCGATTCCT 2205

Qy        697 ValGluAsnThrSerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGln 716

Db       2206 ATTGTA---TCCAATGGTTCCGGACTGTTCAGCTCCTTCTCTATTTTCTCTAAACTGCAA 2262

Qy        717 AlaValTyrAlaArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSer 736

Db       2263 GGATTTTCAGGAACACAGGACGGTTTTGAGGAGAGTTCGGGAGAGATTCGGTCCTTTTCT 2322

Qy        737 AspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPhe--- 755

Db       2323 GCCAGCTCTTTCAGAAATATTTCACTTCCTATAGGAATAACATTTGAAAAAAAATCCCAA 2382

Qy        756 ---AlaGluGlnTyrTyrHisValValAlaMetTyrSerProAspValCysArgSerAsn 774

Db       2383 AAAACACGAACCTACTATTACTTTCTAGGAGCCTACATCCAAGACCTGAAACGTGATGTG 2442

Qy        775 ProLysCysThrThrThrLeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsn 794

Db       2443 GAATCGGGACCTGTAGTGTTACTCAAAAATGCCGTCTCCTGGGATGCTCCTATGGCGAAC 2502

Qy        795 LeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAla 814

Db       2503 TTGGATTCACGAGCCTACATGTTCCGGCTTACGAATCAAAGAGCTCTACACAGACTTCAG 2562

Qy        815 GluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArgSerTyrAsnValAsp 834

Db       2563 ACGCTGTTA---AATGTGTCTTGTGTGCTGCGTGGGCAAAGCCATAGTTACTCCCTGGAT 2619

Qy        835 AlaGlySerLysIleLysPhe 841

Db       2620 CTGGGGACCACTTACAGGTTC 2640

RESULT 10
US-09-620-412C-169
; Sequence 169, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
;  APPLICANT: Steven P. Fling
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
;  TITLE OF INVENTION:  DIAGNOSIS OF CHLAMYDIAL INFECTION
;  FILE REFERENCE: 210121.469C7
;  CURRENT APPLICATION NUMBER: US/09/620,412C
;  CURRENT FILING DATE:  2000-07-20
;  NUMBER OF SEQ ID NOS: 363
;  SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 169
;   LENGTH: 2643
;   TYPE: DNA
;   ORGANISM: Chlamydia
US-09-620-412C-169
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Alignment Scores:
Pred. No.:                1.76e-66      Length:          2643
Score:                    711.50        Matches:         241
Percent Similarity:       44.75%        Conservative:    138
Best Local Similarity:    28.45%        Mismatches:      347
Query Match:              16.57%        Indels:          121
DB:                       4             Gaps:            31

US-09-830-446-27 (1-841) x US-09-620-412C-169 (1-2643)

Qy         41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60

Db        325 TCCTTCACAGATTGCTCTTCCAAGGAAAGCTCT-------------------------- 357

Qy         61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGln------------ 76

Db        358 ---CCTTCTATTATTCATCAA---------AAGAATGGTCAGTTATCCTTGCGCAATAAT 405

Qy         77 ---SerThrSerCysPheLysAsn-----------------AspAlaAlaAlaGlyAsp 89

Db        406 GGTAGCATGAGTTTCTGTCGAAATCATGCTGAAGGCTCTGGAGGAGCCATCTCTGCGGAT 465

Qy         90 LeuAsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThrAla 109

Db        466 GCCTTTTCTCTACAGCACAACTATCTTTTCACAGCTTTTGAAGAGAATTCTTCTAAAGGA 525

Qy        110 SerGlyAlaAlaIleGlySerGluAlaAlaAsnLysThrValThrLeuSer---GlyPhe 128

Db        526 AATGGCGGAGCCATTCAGGCTCAA-----------ACCTTCTCTTTATCTAGAAATGTG 573

Qy        129 SerAlaLeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIle 148

Db        574 TCGCCTATTTCTTTCGCCCGTAATCGTGCGGAT------TTAAATGGC---GGCGCTATT 624

Qy        149 AsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsnPhe 168

Db        625 ---TGCTGTAGTAATCTTATTTGTTCAGGGAATGTAAACCCTCTCTTTTTCACTGGAAAC 681

Qy        169 SerThrGlyAspGlyGlyAlaIleAsnCys----------------------AlaGly 180

Db        682 TCCGCCACGAATGGAGGCGCTATTTGTTGTATCAGCGATCTAAACACCTCAGAAAAAGGC 741

Qy        181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArg 200

Db        742 TCTCTCTCTCTTGCTTGTAACCAAGAAACGCTATTTGCAAGCAATTCTGCTAAAGAAAAA 801

Qy        201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220

Db        802 GGCGGGGCTATTTATGCCAAGCACATGGTATTGCGTTATAACGGTCCTGTTTCCTTCATT 861

Qy        221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240

Db        862 AACAACAGCGCTAAAATA-----------GGTGGAGCTATCGCCATCCAGTCCGGAGGG 909

Qy        241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThr------Ile 258

Db        910 AGTCTCTCTATCCTTGCAGGTGAAGGATCTGTTCTGTTCCAGAATAACTCCCAACGCACC 969

Qy        259 GlyAlaThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThr 278

Db        970 TCCGACCAAGGTCTAGTA---AGAAACGCCATCTACTTARAGAAAGATGCGATTCTTTCT 1026

Qy        279 AlaLeuArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGly 298

Db       1027 TCCTTAGAAGCTCGCAACGGA---GATATTCTTTTCTTTGATCCTATT---GTACAAGAA 1080

Qy        299 SerThrSerValAlaAspAlaLeu-----------------AsnIleAsnSerPro--- 311

Db       1081 AGTAGCAGCAAAGAATCGCCTCTTCCCTCCTCTTTGCAAGCCAGCGTGACTTCTCCCACC 1140

Qy        312 -------------------------AspThrGlyAspAsnLysGluTyrThrGlyThr 322
```

```
Db       1141 CCAGCCACCGCATCTCCTTTAGTTATTCAGACAAGTGCAAACCGT-----------TCA 1188

Qy        323 IleValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThr 342
              ::::::||||||   |||:::|||:::|||   |||   |||         |||   |||
Db       1189 GTGATTTTCTCGAGCGAACGTCTTTCTGAA---GAAGAAAAAACTCCTGATAACCTCACT 1245

Qy        343 SerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspVal 362
              |||:::|||   |||   :::       |||:::|||   :::|||||||||
Db       1246 TCCCAACTACAGCAGCCTATCGAACTGAAATCCGGACGCTTAGTTTTAAAAGATCGCGCT 1305

Qy        363 ValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGly 382
              ||||||||||||          |||||||||      :::   |||||||||:::   |||
Db       1306 GTCCTTTCCGCGCCTTCTCTCTCTCAGGATCCTCAAGCTCTCCTCATTATGGAAGCGGGA 1365

Qy        383 ThrSerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAsp 402
              |||||||||       :::::::::   ::::::|||         |||   |||   :::
Db       1366 ACTTCTTTAAAAACTTCCTCTGAT---TTGAAGTTAGCTACGCTAAGTATTCCCCTTCAT 1422

Qy        403 SerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArg 422
              ||||||          |||   :::   :::   |||                ::::::
Db       1423 TCCTTAGATACTGAAAAAAGCGTAACTATCCACGCC-----------CCTAATCTTTCT 1470

Qy        423 IleAspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsn---GlyPhe 441
              |||   :::       :::             ||||||:::||||||:::|||
Db       1471 ATCCAAAAGATCTTCCTCTCTAACTCTGGAGATGAGAATTTTTATGAAAATGTAGAGCTT 1530

Qy        442 LeuAsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleVal 461
              |||:::::::::   :::         :::|||   |||     :::     :::
Db       1531 CTCAGTAAAGAGCAAAACAATATTCCTCTCCTTACTCTCCCTAAAGAGCAATCTCATTTA 1590

Qy        462 IleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGlyLys 481
                    |||                 :::   |||   :::||||||||||||
Db       1591 CATCTTCCTGATGGGAAC-----------CTCTCTTCTCACTTTGGATATCAAGGAGAT 1638

Qy        482 TrpThrIleAsnTrpSerThrAspAspLys------LysAlaThrValSerTrpAlaLys 499
              ||||||   :::|||           |||:::                  :::|||
Db       1639 TGGACTTTTTCTTGGAAAGATTCTGATGAAGGGCATTCTCTGATTGCTAATTGGACGCCT 1698

Qy        500 GlnSerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGly 519
              :::::::::   |||       |||:::::::::   ||||||   |||   ||||||
Db       1699 AAAAACTATGTGCCTCATCCAGAACGTCAATCTACACTCGTTGCGAACACTCTTTGGAAC 1758

Qy        520 SerPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaPro 539
              ::::::   |||:::::::::   |||:::   |||                  |||
Db       1759 ACCTATTCCGATATGCAAGCTGTGCAGTCGATGATTAATACAACAGCGCACGGAGGAGCC 1818

Qy        540 TyrGluLysArgPheTrpValAlaGlyIleSerAsnVal------LeuHisArgSerGly 557
              |||             |||   :::   :::||||||:::      :::|||   |||
Db       1819 TATCTATTTGGAACGTGGGGATCTGCTGTTTCTAATTTATTCTATGTTCACGACAGCTCT 1878

Qy        558 ArgGluAsnGlnArgLysPheArgHisValSerGlyGlyAlaValValGlyAlaSerThr 577
              :::           :::   |||   |||   |||   :::   |||   ||||||
Db       1879 GGGAAACCTATCGATAATTGGCATCATAGAAGCCTTGGCTACCTATTCGGTATCAGTACT 1938

Qy        578 ArgMetProGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLys 597
                    :::       |||         ||||||      :::
Db       1939 CACAGTTTAGATGACCATTCTTTCTGCTTGGCTGCAGGACAATTACTCGGGAAATCGTCC 1998

Qy        598 AspTyrPheMetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHis 617
              |||   |||:::   :::             :::|||      :::::::::   |||
Db       1999 GATTCCTTTATTACGTCTACAGAAACGACCTCCTATATAGCTACTGTACAAGCGCAACTC 2058

Qy        618 AspAlaSerLeuTyrSerValValSerIleLeuGluGlyGluGlyGlyLeuArgGluIle 637
              ||||||      :::   :::
Db       2059 GCTACCTCTCTAATGAAAATCTCTGCA------------------------------ 2085

Qy        638 LeuLeuProTyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGly 657
                                                        |||       |||
Db       2086 ----------------------------------------CAGGCATGCTACAAT 2100

Qy        658 HisThrAspHisArgMetLysThrGluSerLeuProProProProProThrLeuSerThr 677
                 :::   |||   :::||||||:::                  :::   |||
Db       2101 GAAAGTATCCATGAGCTAAAAACAAAATAT--------------CGCTCCTTCTCTAAA 2145
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```
Qy        678 Asp---HisThrSerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAla 696
                  :::         ||||||                :::|||||:::         :::
Db       2146 GAAGGATTCGGATCCTGGCATAGCGTTGCAGTATCCGGAGAAGTGTGCGCATCGATTCCT 2205

Qy        697 ValGluAsnThrSerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGln 716
              :::       ::::::|||   |||   |||       ::::::   |||   |||:::|||
Db       2206 ATTGTA---TCCAATGGTTCCGGACTGTTCAGCTCCTTCTCTATTTTCTCTAAACTGCAA 2262

Qy        717 AlaValTyrAlaArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSer 736
                          ||||||   |||   |||                  |||   ||||||
Db       2263 GGATTTTCAGGAACACAGGACGGTTTTGAGGAGAGTTCGGGAGAGATTCGGTCCTTTTCT 2322

Qy        737 AspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPhe--- 755
              |||         |||:::::::::|||:::|||||       ||||||:::
Db       2323 GCCAGCTCTTTCAGAAATATTTCACTTCCTATAGGAATAACATTTGAAAAAAAATCCCAA 2382

Qy        756 ---AlaGluGlnTyrTyrHisValValAlaMetTyrSerProAspValCysArgSerAsn 774
                        ||||||:::   :::       |||       |||:::   |||
Db       2383 AAAACACGAACCTACTATTACTTTCTAGGAGCCTACATCCAAGACCTGAAACGTGATGTG 2442

Qy        775 ProLysCysThrThrThrLeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsn 794
                          ||||||   |||       ||||||                :::|||
Db       2443 GAATCGGGACCTGTAGTGTTACTCAAAAATGCCGTCTCCTGGGATGCTCCTATGGCGAAC 2502

Qy        795 LeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAla 814
              |||       :::|||   :::   :::   :::       |||:::|||
Db       2503 TTGGATTCACGAGCCTACATGTTCCGGCTTACGAATCAAAGAGCTCTACACAGACTTCAG 2562

Qy        815 GluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArgSerTyrAsnValAsp 834
              |||     |||                 ||||||   |||   ||||||::::::|||
Db       2563 ACGCTGTTA---AATGTGTCTTGTGTGCTGCGTGGGCAAAGCCATAGTTACTCCCTGGAT 2619

Qy        835 AlaGlySerLysIleLysPhe 841
                |||:::      :::|||
Db       2620 CTGGGGACCACTTACAGGTTC 2640
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RESULT 11
US-09-598-419-169
; Sequence 169, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 169
;   LENGTH: 2643
;   TYPE: DNA
;   ORGANISM: Chlamydia
US-09-598-419-169

Alignment Scores:

Pred. No.:	1.76e-66	Length:	2643
Score:	711.50	Matches:	241
Percent Similarity:	44.75%	Conservative:	138
Best Local Similarity:	28.45%	Mismatches:	347
Query Match:	16.57%	Indels:	121
DB:	4	Gaps:	31

US-09-830-446-27 (1-841) x US-09-598-419-169 (1-2643)

```
Qy         41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
              |||   |||       |||||||||   ||||||
Db        325 TCCTTCACAGATTGCTCTTCCAAGGAAAGCTCT-------------------------- 357

Qy         61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGln------------ 76
                  |||::::::   :::         |||   |||:::
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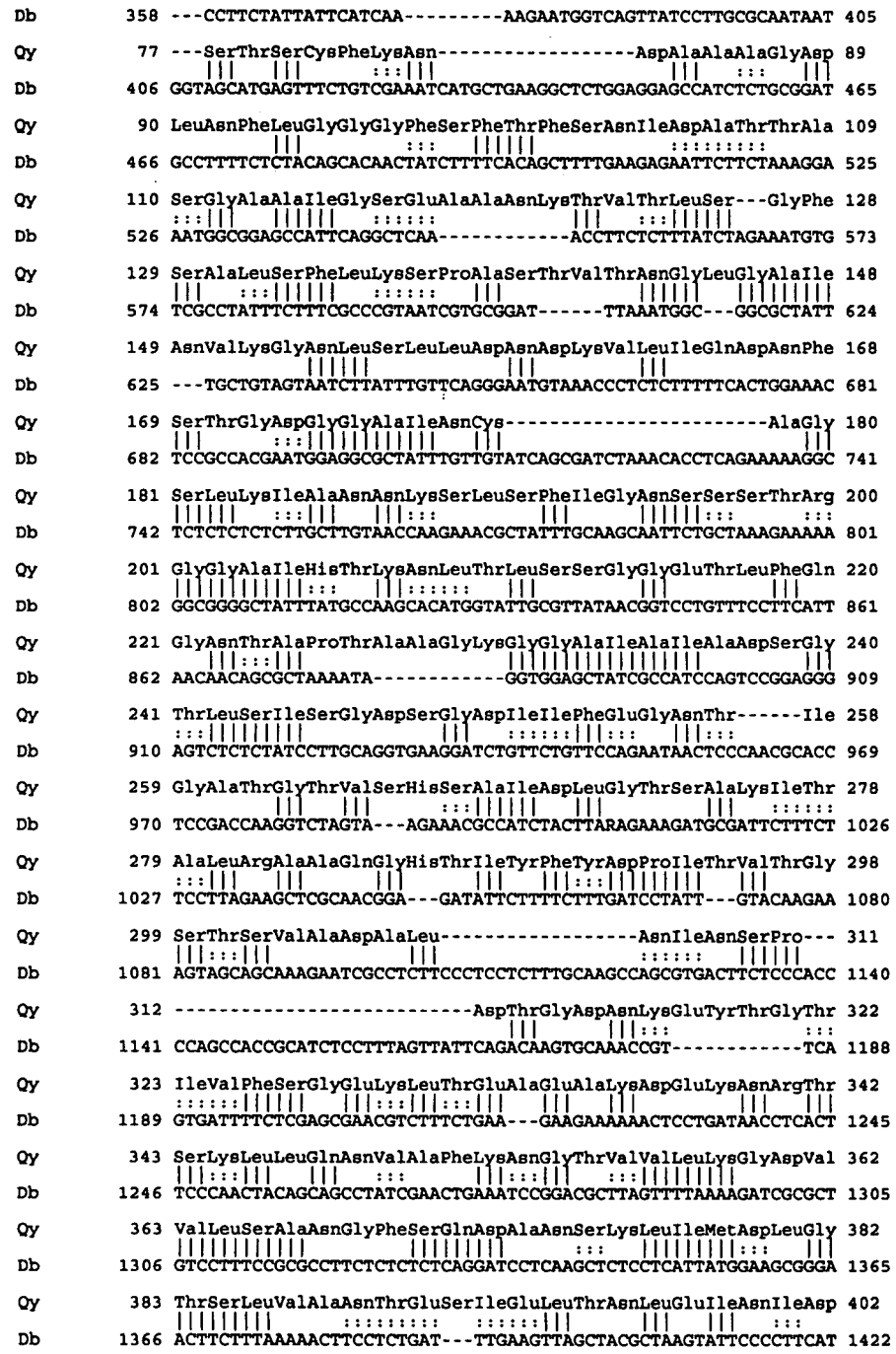

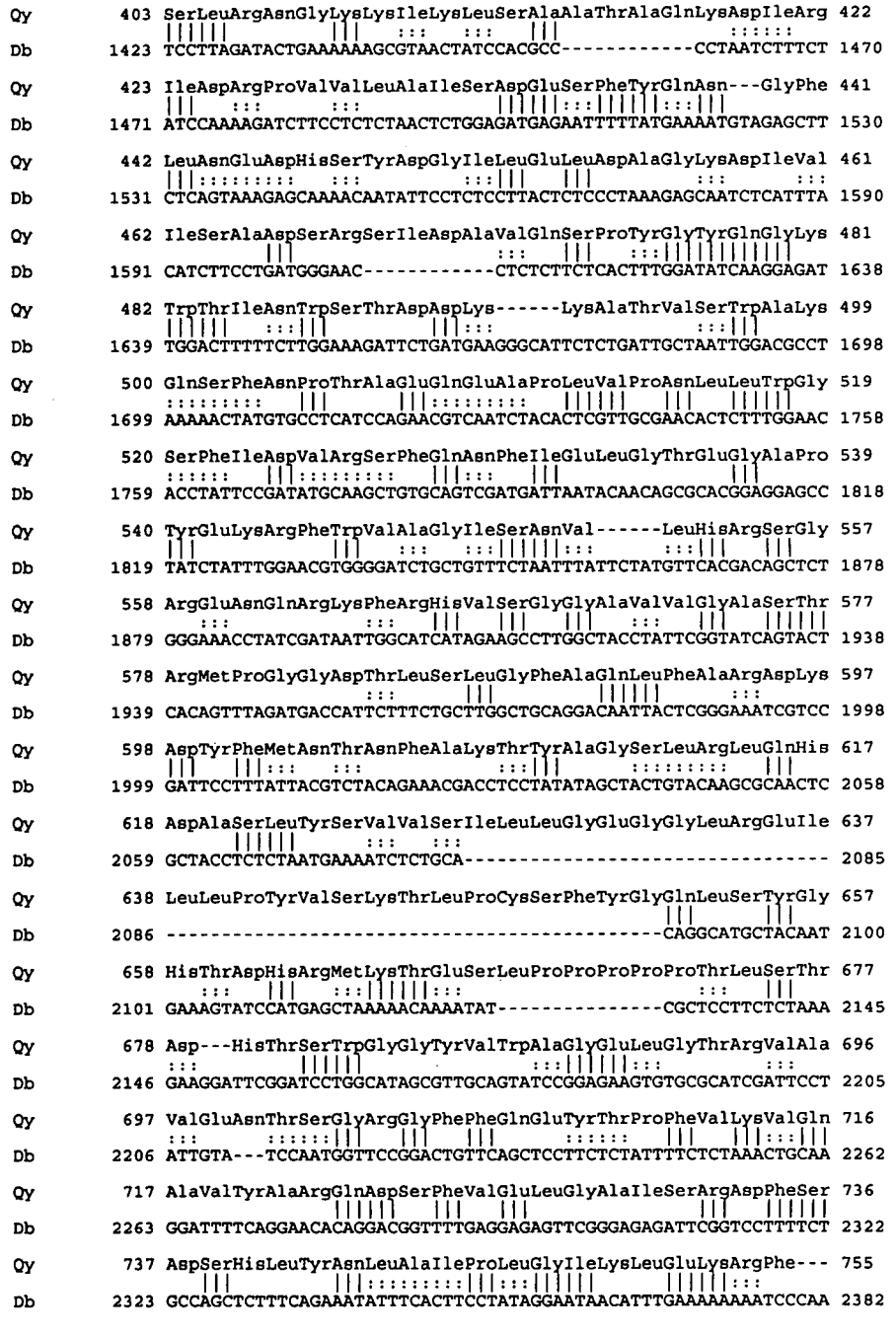

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Qy        756 ---AlaGluGlnTyrTyrHisValValAlaMetTyrSerProAspValCysArgSerAsn 774
Db       2383 AAAACACGAACCTACTATTACTTTCTAGGAGCCTACATCCAAGACCTGAAACGTGATGTG 2442

Qy        775 ProLysCysThrThrThrLeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsn 794
Db       2443 GAATCGGGACCTGTAGTGTTACTCAAAAATGCCGTCTCCTGGGATGCTCCTATGGCGAAC 2502

Qy        795 LeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAla 814
Db       2503 TTGGATTCACGAGCCTACATGTTCCGGCTTACGAATCAAAGAGCTCTACACAGACTTCAG 2562

Qy        815 GluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArgSerTyrAsnValAsp 834
Db       2563 ACGCTGTTA---AATGTGTCTTGTGTGCTGCGTGGGCAAAGCCATAGTTACTCCCTGGAT 2619

Qy        835 AlaGlySerLysIleLysPhe 841
Db       2620 CTGGGGACCACTTACAGGTTC 2640

RESULT 12
US-09-556-877-181
; Sequence 181, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
;  APPLICANT:  Probst, Peter
;  APPLICANT:  Bhatia, Ajay
;  APPLICANT:  Skeiky, Yasir
;  APPLICANT:  Fling, Steve
;  APPLICANT:  Maisonneuve, Jeff
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR TREATMENT AND
;  TITLE OF INVENTION:  DIAGNOSIS OF CHLAMYDIAL INFECTION
;  FILE REFERENCE:  210121.469C5
;  CURRENT APPLICATION NUMBER: US/09/556,877
;  CURRENT FILING DATE:  2000-04-19
;  NUMBER OF SEQ ID NOS:  305
;  SOFTWARE:  FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 181
;   LENGTH: 2601
;   TYPE: DNA
;   ORGANISM: Chlamydia
US-09-556-877-181

Alignment Scores:
Pred. No.:              7.19e-65      Length:          2601
Score:                  696.50        Matches:         238
Percent Similarity:     44.27%        Conservative:    137
Best Local Similarity:  28.10%        Mismatches:      351
Query Match:            16.22%        Indels:          121
DB:                     4             Gaps:            31

US-09-830-446-27 (1-841) x US-09-556-877-181 (1-2601)

Qy         41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
Db        283 TCCTTCACAGATTGCTCTTCCAAGGAAAGCTCT-------------------------- 315

Qy         61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGln----------- 76
Db        316 ---CCTTCTATTATTCATCAA---------AAGAATGGTCAGTTATCCTTGCGCAATAAT 363

Qy         77 ---SerThrSerCysPheLysAsn-----------------AspAlaAlaAlaGlyAsp 89
Db        364 GGTAGCATGAGTTTCTGTCGAAATCATGCTGAAGGCTCTGGAGGAGCCATCTCTGCGGAT 423

Qy         90 LeuAsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThrAla 109
Db        424 GCCTTTTCTCTACAGCACAACTATCTTTTCACAGCTTTTGAAGAGAATTCTTCTAAAGGA 483

Qy        110 SerGlyAlaAlaIleGlySerGluAlaAlaAsnLysThrValThrLeuSer---GlyPhe 128
Db        484 AATGGCGGAGCCATTCAGGCTCAA-----------ACCTTCTCTTTATCTAGAAATGTG 531

Qy        129 SerAlaLeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIle 148
Db        532 TCGCCTATTTCTTTCGCCCGTAATCGTGCGGAT------TTAAATGGC---GGCGCTATT 582

Qy        149 AsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsnPhe 168
Db        583 ---TGCTGTAGTAATCTTATTTGTTCAGGGAATGTAAACCCTCTCTTTTTCACTGGAAAC 639

Qy        169 SerThrGlyAspGlyGlyAlaIleAsnCys----------------------AlaGly 180
Db        640 TCCGCCACRAATGGAGGCSCTATTTGTTGTATCAGCGATCTAAACACCTCAGAAAAAGGC 699

Qy        181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArg 200
Db        700 TCTCTCTCTCTTGCTTGTAACCAARAAACGCTATTTGCAAGCAATTCTGCTAAAGAAAAA 759

Qy        201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220
Db        760 GGCGGGGCTATTTATGCCAAGCACATGGTATTGCGTTATAACGGTCCTGTTTCCTTCATT 819

Qy        221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240
Db        820 AACAACAGCGCTAAAATA-----------GGTGGAGCTATCGCCATCCAGTCCGGAGGG 867

Qy        241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThr------Ile 258
Db        868 AGTCTCTCTATCCTTGCAGGTGAAGGATCTGTTCTGTTCCAGAATAACTCCCAACGCACC 927

Qy        259 GlyAlaThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThr 278
Db        928 TCCGACCAAGGTCTAGTA---AGAAACGCCATCTACTTAGAGAAAGATGCGATTCTTTCT 984

Qy        279 AlaLeuArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGly 298
Db        985 TCCTTAGAAGCTCGCAACGGA---GATATTCTTTTCTTTGATCCTATT---GTACAAGAA 1038

Qy        299 SerThrSerValAlaAspAlaLeu-----------------AsnIleAsnSerPro--- 311
Db       1039 AGTAGCAGCAAAGAATCGCCTCTTCCCTCCTCTTTGCAAGCCAGCGTGACTTCTCCCACC 1098

Qy        312 --------------------------AspThrGlyAspAsnLysGluTyrThrGlyThr 322
Db       1099 CCAGCCACCGCATCTCCTTTAGTTATTCAGACAAGTGCAAACCGT-----------TCA 1146

Qy        323 IleValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThr 342
Db       1147 GTGATTTTCTCGAGCGAACGTCTTTCTGAA---GAAGAAAAAACTCCTGATAACCTCACT 1203

Qy        343 SerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspVal 362
Db       1204 TCCCAACTACAGCAGCCTATCGAACTGAAATCCGGACGCTTAGTTTTAAAAGATCGCGCT 1263

Qy        363 ValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGly 382
Db       1264 GTCCTTTCCGSGCCTTCTCTCTCTCAGGATCCTCAAGCTCTCCTCATTATGGAAGCGGGA 1323

Qy        383 ThrSerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAsp 402
Db       1324 ACTTCTTTAAAAACTTCCTYTGAT---TTGAAGTTAGSTACGSTAAGTATTCCCCTTCAT 1380

Qy        403 SerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArg 422
Db       1381 TCCTTAGATACTGAAAAAAGCGTAACTATCCACGCC------------CCTAATCTTTCT 1428

Qy        423 IleAspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsn---GlyPhe 441
Db       1429 ATCCAAAAGATCTTCCTCTCTAACTCTGGAGATGAGAATTTTTATGAAAATGTAGAGCTT 1488

Qy        442 LeuAsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleVal 461
Db       1489 CTCAGTAAAGAGCAAAACAATATTCCTCTCCTTACTCTCCCTAAAGAGCAATCTCATTTA 1548

Qy        462 IleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGlyLys 481
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Db       1549 CATCTTCCTGATGGGAAC-----------CTCTCTTCTCACTTTGGATATCAAGGAGAT 1596

Qy        482 TrpThrIleAsnTrpSerThrAspAspLys------LysAlaThrValSerTrpAlaLys 499

Db       1597 TGGACTTTTTCTTGGAAAGATTCTGATGAAGGGCATTCTCTGATTGCTAATTGGACGCCT 1656

Qy        500 GlnSerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGly 519

Db       1657 AAAAACTATGTGCCTCATCCAGAACGTCAATCTACACTCGTTGCGAACACTCTTTGGAAC 1716

Qy        520 SerPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaPro 539

Db       1717 ACCTATTCCGATATGCAAGCTGTGCAGTCGATGATTAATACAACAGCGCACGGAGGAGCC 1776

Qy        540 TyrGluLysArgPheTrpValAlaGlyIleSerAsnVal------LeuHisArgSerGly 557

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Qy        578 ArgMetProGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLys 597

Db       1897 CACAGTTTAGATGACCATTCTTTCTGCTTGGCTGCAGGACAATTACTCGGGAAATCGTCC 1956

Qy        598 AspTyrPheMetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHis 617

Db       1957 GATTCCTTTATTACGTCTACAGAAACGACCTCCTATATAGCTACTGTACAAGCGCAACTC 2016

Qy        618 AspAlaSerLeuTyrSerValValSerIleLeuGlyGluGlyGlyLeuArgGluIle 637

Db       2017 GCTACCTCTCTAATGAAAATCTCTGCA------------------------------ 2043

Qy        638 LeuLeuProTyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGly 657

Db       2044 ----------------------------------------CAGGCATGCTACAAT 2058

Qy        658 HisThrAspHisArgMetLysThrGluSerLeuProProProProProThrLeuSerThr 677

Db       2059 GAAAGTATCCATGAGCTAAAAACAAAATAT--------------CGCTCCTTCTCTAAA 2103

Qy        678 Asp---HisThrSerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAla 696

Db       2104 GAAGGATTCGGATCCTGGCATAGCGTTGCAGTATCCGGAGAAGTGTGCGCATCGATTCCT 2163

Qy        697 ValGluAsnThrSerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGln 716

Db       2164 ATTGTA---TCCAATGGTTCCGGACTGTTCAGCTCCTTCTCTATTTTCTCTAAACTGCAA 2220

Qy        717 AlaValTyrAlaArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSer 736

Db       2221 GGATTTTCAGGAACACAGGACGGTTTTGAGGAGAGTTCGGGAGAGATTCGGTCCTTTTCT 2280

Qy        737 AspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPhe--- 755

Db       2281 GCCAGCTCTTTCAGAAATATTTCACTTCCTATAGGAATAACATTTGAAAAAAAATCCCAA 2340

Qy        756 ---AlaGluGlnTyrTyrHisValValAlaMetTyrSerProAspValCysArgSerAsn 774

Db       2341 AAAACACGAACCTACTATTACTTTCTAGGAGCCTACATCCAAGACCTGAAACGTGATGTG 2400

Qy        775 ProLysCysThrThrThrLeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsn 794

Db       2401 GAATCGGGACCTGTAGTGTTACTCAAAAATGCCGTCTCCTGGGATGCTCCTATGGCGAAC 2460

Qy        795 LeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAla 814

Db       2461 TTGGATTCACGAGCCTACATGTTCCGGCTTACGAATCAAAGAGCTCTACACAGACTTCAG 2520

Qy        815 GluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArgSerTyrAsnValAsp 834

Db       2521 ACGCTGTTA---AATGTGTCTTGTGTGCTGCGTGGGCAAAGCCATAGTTACTCCCTGGAT 2577

Qy        835 AlaGlySerLysIleLysPhe 841

Db       2578 CTGGGGACCACTTACAGGTTC 2598

RESULT 13
US-09-620-412C-181
; Sequence 181, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
;  APPLICANT: Steven P. Fling
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
;  TITLE OF INVENTION:  DIAGNOSIS OF CHLAMYDIAL INFECTION
;  FILE REFERENCE: 210121.469C7
;  CURRENT APPLICATION NUMBER: US/09/620,412C
;  CURRENT FILING DATE:  2000-07-20
;  NUMBER OF SEQ ID NOS: 363
;  SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 181
;   LENGTH: 2601
;   TYPE: DNA
;   ORGANISM: Chlamydia
US-09-620-412C-181

Alignment Scores:
Pred. No.:              7.19e-65        Length:         2601
Score:                  696.50          Matches:        238
Percent Similarity:     44.27%          Conservative:   137
Best Local Similarity:  28.10%          Mismatches:     351
Query Match:            16.22%          Indels:         121
DB:                     4               Gaps:           31

US-09-830-446-27 (1-841) x US-09-620-412C-181 (1-2601)

Qy         41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60

Db        283 TCCTTCACAGATTGCTCTTCCAAGGAAAGCTCT------------------------- 315

Qy         61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGln----------- 76

Db        316 ---CCTTCTATTATTCATCAA---------AAGAATGGTCAGTTATCCTTGCGCAATAAT 363

Qy         77 ---SerThrSerCysPheLysAsn-----------------AspAlaAlaAlaGlyAsp 89

Db        364 GGTAGCATGAGTTTCTGTCGAAATCATGCTGAAGGCTCTGGAGGAGCCATCTCTGCGGAT 423

Qy         90 LeuAsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThrAla 109

Db        424 GCCTTTTCTCTACAGCACAACTATCTTTTCACAGCTTTTGAAGAGAATTCTTCTAAAGGA 483

Qy        110 SerGlyAlaAlaIleGlySerGluAlaAlaAsnLysThrValThrLeuSer---GlyPhe 128

Db        484 AATGGCGGAGCCATTCAGGCTCAA-----------ACCTTCTCTTTATCTAGAAATGTG 531

Qy        129 SerAlaLeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIle 148

Db        532 TCGCCTATTTCTTTCGCCCGTAATCGTGCGGAT------TTAAATGGC---GGCGCTATT 582

Qy        149 AsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsnPhe 168

Db        583 ---TGCTGTAGTAATCTTATTTGTTCAGGGAATGTAAACCCTCTCTTTTTCACTGGAAAC 639

Qy        169 SerThrGlyAspGlyGlyAlaIleAsnCys----------------------AlaGly 180

Db        640 TCCGCCACRAATGGAGGCSCTATTTGTTGTATCAGCGATCTAAACACCTCAGAAAAAGGC 699

Qy        181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArg 200

Db        700 TCTCTCTCTCTTGCTTGTAACCAARAAACGCTATTTGCAAGCAATTCTGCTAAAGAAAAA 759

Qy        201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220
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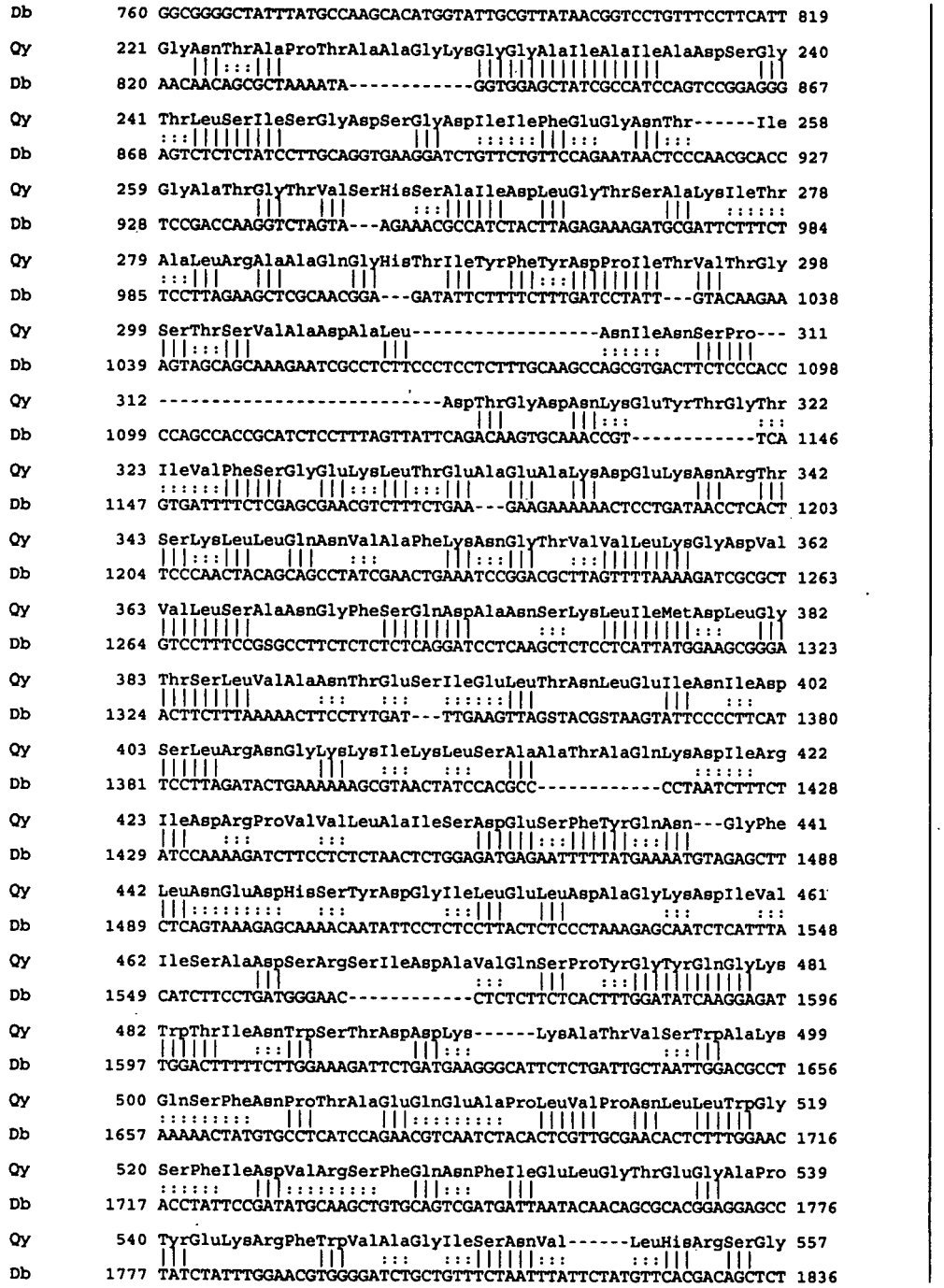

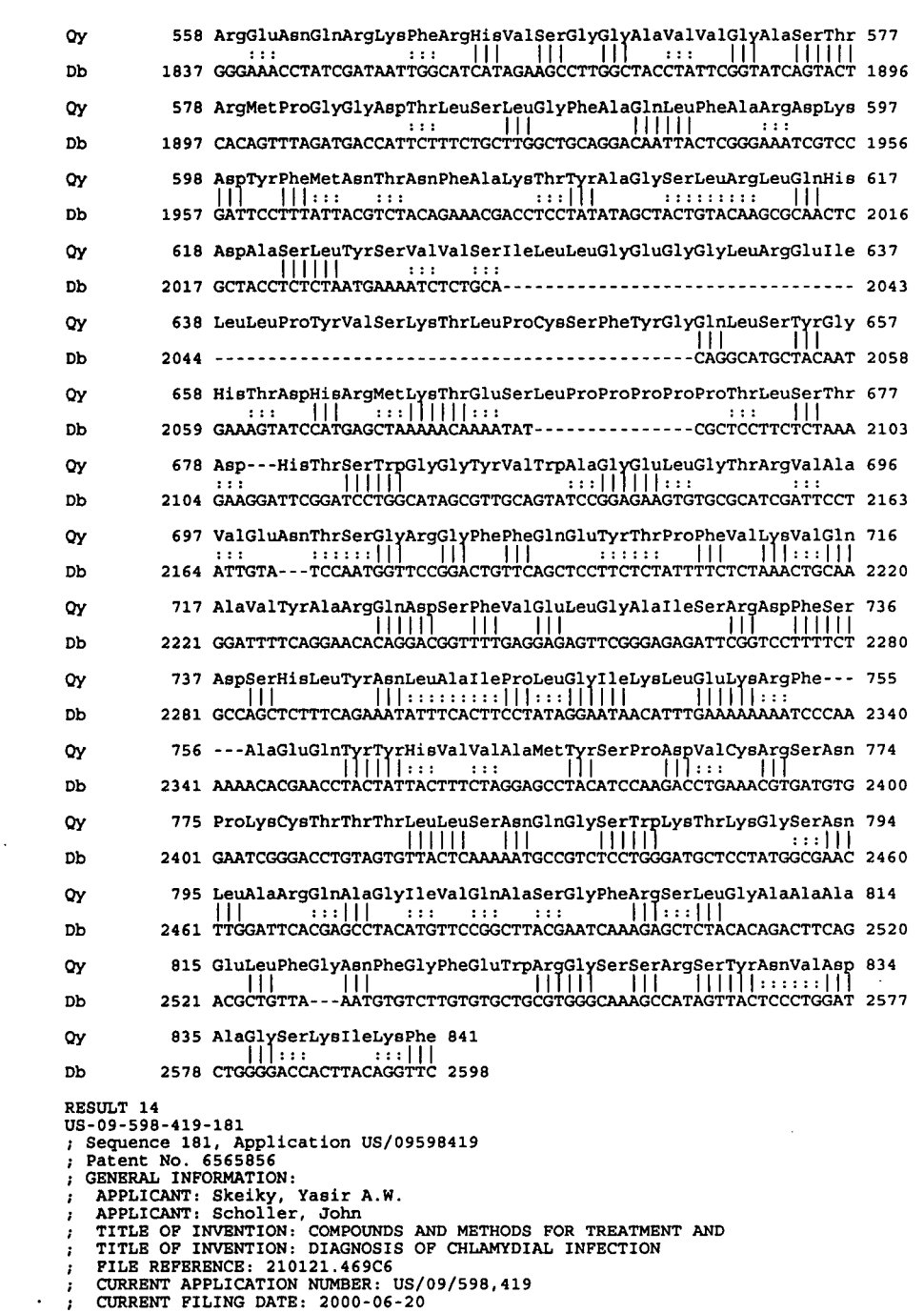

RESULT 14
US-09-598-419-181
; Sequence 181, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20

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;  NUMBER OF SEQ ID NOS: 357
;  SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 181
;    LENGTH: 2601
;    TYPE: DNA
;    ORGANISM: Chlamydia
US-09-598-419-181

Alignment Scores:
Pred. No.:                  7.19e-65        Length:         2601
Score:                      696.50          Matches:        238
Percent Similarity:         44.27%          Conservative:   137
Best Local Similarity:      28.10%          Mismatches:     351
Query Match:                16.22%          Indels:         121
DB:                         4               Gaps:           31

US-09-830-446-27 (1-841) x US-09-598-419-181 (1-2601)

Qy         41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
Db        283 TCCTTCACAGATTGCTCTTCCAAGGAAAGCTCT--------------------------- 315

Qy         61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGln------------ 76
Db        316 ---CCTTCTATTATTCATCAA---------AAGAATGGTCAGTTATCCTTGCGCAATAAT 363

Qy         77 ---SerThrSerCysPheLysAsn-----------------AspAlaAlaAlaGlyAsp 89
Db        364 GGTAGCATGAGTTTCTGTCGAAATCATGCTGAAGGCTCTGGAGGAGCCATCTCTGCGGAT 423

Qy         90 LeuAsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThrAla 109
Db        424 GCCTTTTCTCTACAGCACAACTATCTTTTCACAGCTTTTGAAGAGAATTCTTCTAAAGGA 483

Qy        110 SerGlyAlaAlaIleGlySerGluAlaAlaAsnLysThrValThrLeuSer---GlyPhe 128
Db        484 AATGGCGGAGCCATTCAGGCTCAA------------ACCTTCTCTTTATCTAGAAATGTG 531

Qy        129 SerAlaLeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIle 148
Db        532 TCGCCTATTTCTTTCGCCCGTAATCGTGCGGAT------TTAAATGGC---GGCGCTATT 582

Qy        149 AsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsnPhe 168
Db        583 ---TGCTGTAGTAATCTTATTTGTTCAGGGAATGTAAACCCTCTCTTTTTCACTGGAAAC 639

Qy        169 SerThrGlyAspGlyGlyAlaIleAsnCys----------------------AlaGly 180
Db        640 TCCGCCACRAATGGAGGCSCTATTTGTTGTATCAGCGATCTAAACACCTCAGAAAAAGGC 699

Qy        181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArg 200
Db        700 TCTCTCTCTCTTGCTTGTAACCAARAAACGCTATTTGCAAGCAATTCTGCTAAAGAAAAA 759

Qy        201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220
Db        760 GGCGGGGCTATTTATGCCAAGCACATGGTATTGCGTTATAACGGTCCTGTTTCCTTCATT 819

Qy        221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240
Db        820 AACAACAGCGCTAAAATA-----------GGTGGAGCTATCGCCATCCAGTCCGGAGGG 867

Qy        241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThr------Ile 258
Db        868 AGTCTCTCTATCCTTGCAGGTGAAGGATCTGTTCTGTTCCAGAATAACTCCCAACGCACC 927

Qy        259 GlyAlaThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThr 278
Db        928 TCCGACCAAGGTCTAGTA---AGAAACGCCATCTACTTAGAGAAAGATGCGATTCTTTCT 984

Qy        279 AlaLeuArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGly 298
Db        985 TCCTTAGAAGCTCGCAACGGA---GATATTCTTTTCTTTGATCCTATT---GTACAAGAA 1038

Qy        299 SerThrSerValAlaAspAlaLeu-----------------AsnIleAsnSerPro--- 311
Db       1039 AGTAGCAGCAAAGAATCGCCTCTTCCCTCCTCTTTGCAAGCCAGCGTGACTTCTCCCACC 1098

Qy        312 --------------------------AspThrGlyAspAsnLysGluTyrThrGlyThr 322
Db       1099 CCAGCCACCGCATCTCCTTTAGTTATTCAGACAAGTGCAAACCGT------------TCA 1146

Qy        323 IleValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThr 342
Db       1147 GTGATTTTCTCGAGCGAACGTCTTTCTGAA---GAAGAAAAAACTCCTGATAACCTCACT 1203

Qy        343 SerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspVal 362
Db       1204 TCCCAACTACAGCAGCCTATCGAACTGAAATCCGGACGCTTAGTTTTAAAAGATCGCGCT 1263

Qy        363 ValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGly 382
Db       1264 GTCCTTTCCGSGCCTTCTCTCTCTCAGGATCCTCAAGCTCTCCTCATTATGGAAGCGGGA 1323

Qy        383 ThrSerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAsp 402
Db       1324 ACTTCTTTAAAAACTTCCTYTGAT---TTGAAGTTAGSTACGSTAAGTATTCCCCTTCAT 1380

Qy        403 SerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArg 422
Db       1381 TCCTTAGATACTGAAAAAAGCGTAACTATCCACGCC------------CCTAATCTTTCT 1428

Qy        423 IleAspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsn---GlyPhe 441
Db       1429 ATCCAAAAGATCTTCCTCTCTAACTCTGGAGATGAGAATTTTTATGAAAATGTAGAGCTT 1488

Qy        442 LeuAsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleVal 461
Db       1489 CTCAGTAAAGAGCAAAACAATATTCCTCTCCTTACTCTCCCTAAAGAGCAATCTCATTTA 1548

Qy        462 IleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGlyLys 481
Db       1549 CATCTTCCTGATGGGAAC------------CTCTCTTCTCACTTTGGATATCAAGGAGAT 1596

Qy        482 TrpThrIleAsnTrpSerThrAspAspLys------LysAlaThrValSerTrpAlaLys 499
Db       1597 TGGACTTTTTCTTGGAAAGATTCTGATGAAGGGCATTCTCTGATTGCTAATTGGACGCCT 1656

Qy        500 GlnSerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGly 519
Db       1657 AAAAACTATGTGCCTCATCCAGAACGTCAATCTACACTCGTTGCGAACACTCTTTGGAAC 1716

Qy        520 SerPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaPro 539
Db       1717 ACCTATTCCGATATGCAAGCTGTGCAGTCGATGATTAATACAACAGCGCACGGAGGAGCC 1776

Qy        540 TyrGluLysArgPheTrpValAlaGlyIleSerAsnVal------LeuHisArgSerGly 557
Db       1777 TATCTATTTGGAACGTGGGGATCTGCTGTTTCTAATTTATTCTATGTTCACGACAGCTCT 1836

Qy        558 ArgGluAsnGlnArgLysPheArgHisValSerGlyGlyAlaValValGlyAlaSerThr 577
Db       1837 GGGAAACCTATCGATAATTGGCATCATAGAAGCCTTGGCTACCTATTCGGTATCAGTACT 1896

Qy        578 ArgMetProGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLys 597
Db       1897 CACAGTTTAGATGACCATTCTTTCTGCTTGGCTGCAGGACAATTACTCGGGAAATCGTCC 1956

Qy        598 AspTyrPheMetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHis 617
Db       1957 GATTCCTTTATTACGTCTACAGAAACGACCTCCTATATAGCTACTGTACAAGCGCAACTC 2016

Qy        618 AspAlaSerLeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIle 637
Db       2017 GCTACCTCTCTAATGAAAATCTCTGCA------------------------------- 2043
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Qy       638 LeuLeuProTyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGly 657
Db      2044 ----------------------------------------------CAGGCATGCTACAAT 2058

Qy       658 HisThrAspHisArgMetLysThrGluSerLeuProProProProProThrLeuSerThr 677
Db      2059 GAAAGTATCCATGAGCTAAAAACAAAATAT--------------CGCTCCTTCTCTAAA 2103

Qy       678 Asp---HisThrSerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAla 696
Db      2104 GAAGGATTCGGATCCTGGCATAGCGTTGCAGTATCCGGAGAAGTGTGCGCATCGATTCCT 2163

Qy       697 ValGluAsnThrSerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGln 716
Db      2164 ATTGTA---TCCAATGGTTCCGGACTGTTCAGCTCCTTCTCTATTTTCTCTAAACTGCAA 2220

Qy       717 AlaValTyrAlaArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSer 736
Db      2221 GGATTTTCAGGAACACAGGACGGTTTTGAGGAGAGTTCGGGAGAGATTCGGTCCTTTTCT 2280

Qy       737 AspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPhe--- 755
Db      2281 GCCAGCTCTTTCAGAAATATTTCACTTCCTATAGGAATAACATTTGAAAAAAAATCCCAA 2340

Qy       756 ---AlaGluGlnTyrTyrHisValValAlaMetTyrSerProAspValCysArgSerAsn 774
Db      2341 AAAACACGAACCTACTATTACTTTCTAGGAGCCTACATCCAAGACCTGAAACGTGATGTG 2400

Qy       775 ProLysCysThrThrThrLeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsn 794
Db      2401 GAATCGGGACCTGTAGTGTTACTCAAAAATGCCGTCTCCTGGGATGCTCCTATGGCGAAC 2460

Qy       795 LeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAla 814
Db      2461 TTGGATTCACGAGCCTACATGTTCCGGCTTACGAATCAAAGAGCTCTACACAGACTTCAG 2520

Qy       815 GluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArgSerTyrAsnValAsp 834
Db      2521 ACGCTGTTA---AATGTGTCTTGTGTGCTGCGTGGGCAAAGCCATAGTTACTCCCTGGAT 2577

Qy       835 AlaGlySerLysIleLysPhe 841
Db      2578 CTGGGGACCACTTACAGGTTC 2598

RESULT 15
US-09-556-877-171
; Sequence 171, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
;  APPLICANT:  Probst, Peter
;  APPLICANT:  Bhatia, Ajay
;  APPLICANT:  Skeiky, Yasir
;  APPLICANT:  Fling, Steve
;  APPLICANT:  Maisonneuve, Jeff
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR TREATMENT AND
;  TITLE OF INVENTION:  DIAGNOSIS OF CHLAMYDIAL INFECTION
;  FILE REFERENCE:  210121.469C5
;  CURRENT APPLICATION NUMBER: US/09/556,877
;  CURRENT FILING DATE:  2000-04-19
;  NUMBER OF SEQ ID NOS:  305
;  SOFTWARE:  FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 171
;   LENGTH: 2895
;   TYPE: DNA
;   ORGANISM: Chlamydia
US-09-556-877-171

Alignment Scores:
Pred. No.:              1.71e-46        Length:         2895
Score:                  527.50          Matches:        209
Percent Similarity:     37.54%          Conservative:   121
Best Local Similarity:  23.78%          Mismatches:     338
Query Match:            12.28%          Indels:         211

DB:                 4           Gaps:          33

US-09-830-446-27 (1-841) x US-09-556-877-171 (1-2895)

Qy        23 GlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThrSerThr 42
Db       457 GGAGCCATTCATGCTCAAAATCTTTACATAAATCATAATCATGATGTGGTCGGATTTATG 516

Qy        43 ThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsn--------------- 57
Db       517 AAGAACTTTTCTTATGTCCAAGGAGGAGCCATTAGTACCGCTAATACCTTTGTTGTGAGC 576

Qy        58 --------------TyrValPheLysAspSerValValIleGluAsnValProLysThr 72
Db       577 GAGAATCAGTCTTGTTTTCTCTTTATGGACAACATCTGTATTCAAACT------------ 624

Qy        73 GlyGluThrGlnSerThrSerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPhe 92
Db       625 ----------------------------AATACAGCAGGAAAAGGTGGCGCTATCTAT 654

Qy        93 LeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAla 112
Db       655 GCTGGAACGAGCAATTCTTTTGAGAGTAATAACTGCGATCTCTTCTTCATCAATAACGCC 714

Qy       113 AlaIleGlySerGluAlaAlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSer 132
Db       715 TGTTGTGCAGGAGGAGCG----------------------------------------- 732

Qy       133 PheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValLysGly 152
Db       733 ---ATCTTCTCCCCTATCTGTTCTCTAACAGGAAAT-----------------CGTGGT 771

Qy       153 AsnLeuSerLeuLeuAspAsnAsp------LysValLeuIleGlnAspAsnPheSerThr 170
Db       772 AACATCGTTTTCTATAACAATCGCTGCTTTAAAAATGTAGAAACAGCTTCTTCAGAAGCT 831

Qy       171 GlyAspGlyGlyAlaIleAsnCysAlaGlySerLeuLysIleAlaAsnAsnLysSer--- 189
Db       832 TCTGATGGAGGAGCAATTAAAGTAACTACTCGCCTAGATGTTACAGGCAATCGTGGTAGG 891

Qy       190 LeuSerPheIleGlyAsnSerSerSerThrArgGlyGlyAlaIleHisThrLysAsnLeu 209
Db       892 ATCTTTTTAGTGACAATATCACAAAAAATTATGGCGGAGCTATTTACGCTCCTGTAGTT 951

Qy       210 ThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGly 229
Db       952 ACCCTAGTGGATAATGGCCCTACCTACTTTATAAACAAT---------ATCGCCAATAAT 1002

Qy       230 LysGlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGly 249
Db      1003 AAGGGGGGCGCTATCTATATAGACGGAACCAGTAACTCCAAAATTTCTGCCGACCGCCAT 1062

Qy       250 AspIleIlePheGluGlyAsnThrIle-----------GlyAlaThrGlyThrValSer 265
Db      1063 GCTATTATTTTTAATGAAAATATTGTGACTAATGTAACTAATGCAAATGGTACCAGTACG 1122

Qy       266 -----------------HisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAla 279
Db      1123 TCAGCTAATCCTCCTAGAAGAAATGCAATAACAGTAGCAAGCTCCTCTGGTGAAATTCTA 1182

Qy       280 LeuArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGlySer 299
Db      1183 TTAGGAGCAGGGAGTAGCCAAAATTTAATTTTTTATGATCCTATTGAAGTTAGC---AAT 1239

Qy       300 ThrSerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGluTyr 319
Db      1240 GCAGGGGTCTCTGTGTCCTTCAAT--------------------AAGGAAGCTGATCAA 1278

Qy       320 ThrGlyThrIleValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGluLys 339
Db      1279 ACAGGCTCTGTAGTATTTTCAGGAGCTACTGTTAATTCTGCAGATTTT---CATCAACGC 1335

Qy       340 AsnArgThrSerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLys 359
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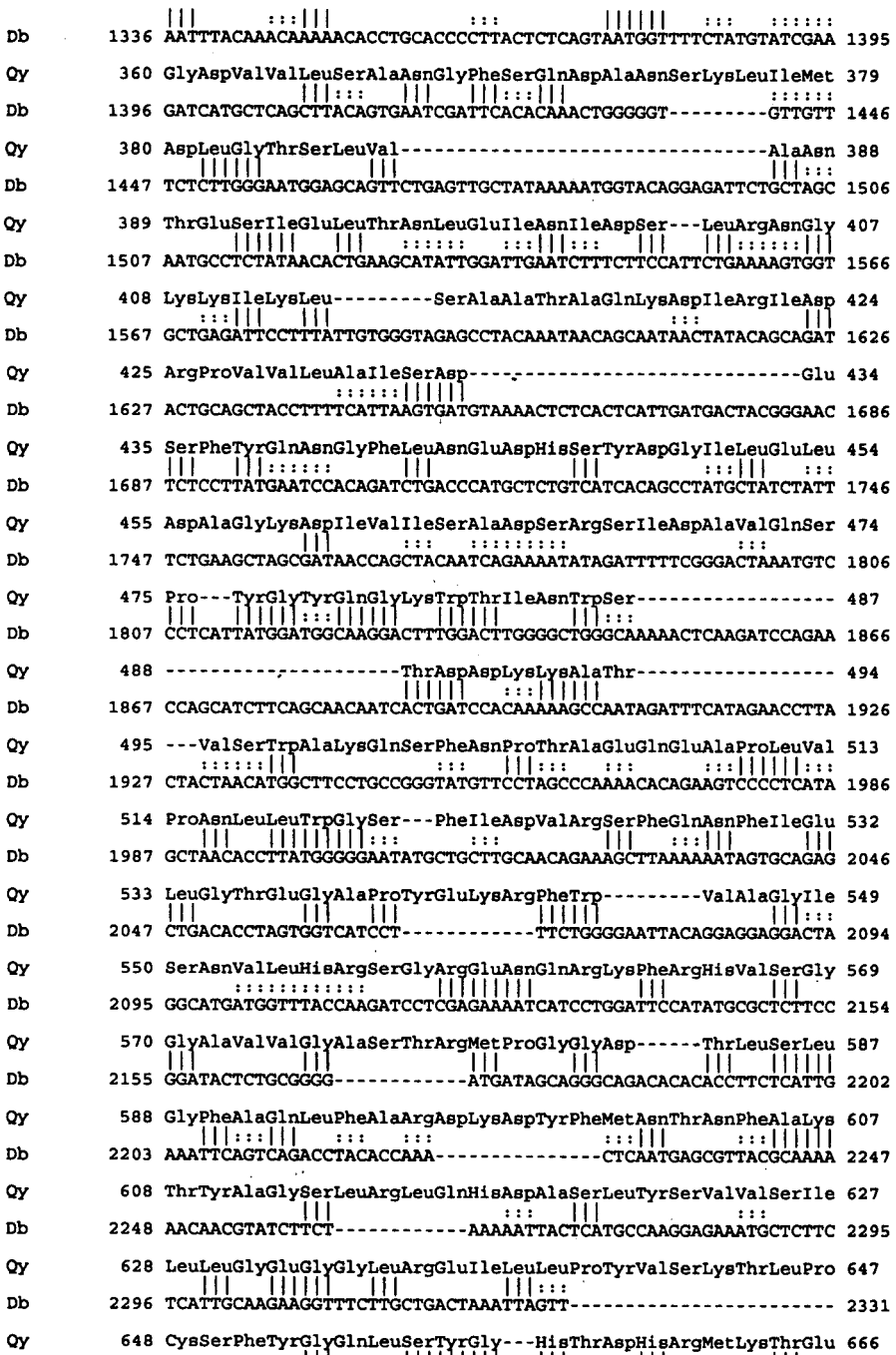

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Job time : 1583 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 29, 2004, 10:21:11 ; Search time 722 Seconds
(without alignments)
4245.252 Million cell updates/sec

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Perfect score: 4295
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2434939 seqs, 1822278265 residues

Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09830446_@CGN_1_1_469_@runat_29012004_102103_19252
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4295	100.0	2526	12	US-10-312-273-140	Sequence 140, App
2	4255	99.1	1230025	12	US-10-289-762-1	Sequence 1, Appli
3	1580.5	36.8	3000	13	US-09-428-122-1	Sequence 1, Appli
4	1497	34.9	2520	13	US-09-738-269-22	Sequence 22, Appl
5	1497	34.9	2520	14	US-10-023-437-22	Sequence 22, Appl
6	1435.5	33.4	2787	12	US-10-312-273-116	Sequence 116, App
7	1415.5	33.0	2793	12	US-10-312-273-46	Sequence 46, Appl
8	1407.5	32.8	2787	12	US-10-312-273-96	Sequence 96, Appl
9	1379.5	32.1	2787	12	US-10-312-273-34	Sequence 34, Appl
c 10	1365	31.8	1230025	12	US-10-289-762-1	Sequence 1, Appli
11	1357.5	31.6	2241	12	US-10-312-273-20	Sequence 20, Appl
12	1335.5	31.1	2811	12	US-10-312-273-154	Sequence 154, App
13	1335.5	31.1	3050	9	US-09-452-380-1	Sequence 1, Appli
14	1335.5	31.1	3050	13	US-10-324-129-1	Sequence 1, Appli
15	1286.5	30.0	2781	13	US-09-738-269-56	Sequence 56, Appl
16	1286.5	30.0	2781	14	US-10-023-437-56	Sequence 56, Appl
17	1279.5	29.8	2808	9	US-09-452-380-2	Sequence 2, Appli
18	1279.5	29.8	2808	13	US-10-324-129-2	Sequence 2, Appli
19	1089	25.4	2922	12	US-10-312-273-4	Sequence 4, Appli
20	1016	23.7	2769	12	US-10-312-273-42	Sequence 42, Appl
21	1011	23.5	2950	9	US-09-886-468-6	Sequence 6, Appli
22	1002	23.3	4224	9	US-09-841-132-486	Sequence 486, App
23	1002	23.3	4224	12	US-10-312-273-32	Sequence 32, Appl
24	939	21.9	3021	9	US-09-841-132-182	Sequence 182, App
25	936	21.8	2949	9	US-09-841-132-170	Sequence 170, App
26	828.5	19.3	2040	13	US-09-738-269-52	Sequence 52, Appl
27	828.5	19.3	2040	14	US-10-023-437-52	Sequence 52, Appl
28	711.5	16.6	2643	9	US-09-841-132-169	Sequence 169, App
29	696.5	16.2	2601	9	US-09-841-132-181	Sequence 181, App
30	648	15.1	1065	12	US-10-312-273-16	Sequence 16, Appl
31	559	13.0	1485	12	US-10-312-273-134	Sequence 134, App
32	557	13.0	1745	9	US-09-886-468-10	Sequence 10, Appl
33	555	12.9	1545	12	US-10-312-273-52	Sequence 52, Appl
34	549.5	12.8	1188	12	US-10-312-273-22	Sequence 22, Appl
35	536.5	12.5	5172	9	US-09-841-132-374	Sequence 374, App
36	536.5	12.5	5172	9	US-09-841-132-375	Sequence 375, App
37	536.5	12.5	5172	12	US-10-312-273-120	Sequence 120, App
38	527.5	12.3	2895	9	US-09-841-132-171	Sequence 171, App
39	527.5	12.3	2934	9	US-09-841-132-183	Sequence 183, App
40	509.5	11.9	3050	10	US-09-779-081-1	Sequence 1, Appli
41	509.5	11.9	4830	12	US-10-312-273-84	Sequence 84, Appl
42	509.5	11.9	4830	13	US-09-841-260-59	Sequence 59, Appl
43	509.5	11.9	4830	14	US-10-007-693-59	Sequence 59, Appl
44	506	11.8	5265	9	US-09-841-132-174	Sequence 174, App
45	502	11.7	5253	9	US-09-841-132-421	Sequence 421, App

ALIGNMENTS

RESULT 1
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; Sequence 140, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035WO
; CURRENT APPLICATION NUMBER: US/10/312,273
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10

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;  PRIOR APPLICATION NUMBER: 0031706.5
;  PRIOR FILING DATE: 2000-12-22
;  NUMBER OF SEQ ID NOS: 664
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 140
;   LENGTH: 2526
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-312-273-140

Alignment Scores:
Pred. No.:                0          Length:          2526
Score:                    4295.00    Matches:         841
Percent Similarity:       100.00%    Conservative:    0
Best Local Similarity:    100.00%    Mismatches:      0
Query Match:              100.00%    Indels:          0
DB:                       12         Gaps:            0

US-09-830-446-27 (1-841) x US-10-312-273-140 (1-2526)

Qy          1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
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Qy         21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
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Db         61 TTATTAGGAGCTGCTACTACCGAAGAGTTATCGGCTAGCAATAGCTTCGATGGAACTACA 120

Qy         41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
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Qy         61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCys 80
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Qy        101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsn 120
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Qy        121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
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Qy        141 ValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAsp 160
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Qy        161 LysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180
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Db        481 AAGGTATTGATTCAGGACAATTTCTCAACAGGAGATGGCGGAGCAATTAATTGTGCAGGC 540

Qy        181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArg 200
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Db        541 TCCTTGAAGATCGCAAACAATAAGTCCCTTTCTTTTATTGGAAATAGTTCTTCAACACGT 600

Qy        201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220
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Qy        221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240
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Db        661 GGGAATACAGCGCCTACGGCTGCTGGTAAAGGAGGTGCTATCGCGATTGCAGACTCTGGC 720

Qy        241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260
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Db        721 ACCCTATCCATTTCTGGAGACAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCT 780

Qy        261 ThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeu 280
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Qy        281 ArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGlySerThr 300
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Db        841 CGTGCTGCGCAAGGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGACA 900

Qy        301 SerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGluTyrThr 320
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Db        901 TCTGTTGCTGATGCTCTCAATATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACG 960

Qy        321 GlyThrIleValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGluLysAsn 340
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Db        961 GGAACCATAGTCTTTTCTGGAGAGAAGCTCACGGAGGCAGAAGCTAAAGATGAGAAGAAC 1020

Qy        341 ArgThrSerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLysGly 360
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Db       1021 CGCACTTCTAAATTACTTCAAAATGTTGCTTTTAAAAATGGGACTGTAGTTTTAAAAGGT 1080

Qy        361 AspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAsp 380
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Db       1081 GATGTCGTTTTAAGTGCGAACGGTTTCTCTCAGGATGCAAACTCTAAGTTGATTATGGAT 1140

Qy        381 LeuGlyThrSerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsn 400
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Qy        401 IleAspSerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAsp 420
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Db       1201 ATAGACTCTCTCAGGAACGGGAAAAAGATAAAACTCAGTGCTGCCACAGCTCAGAAAGAT 1260

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Db       1261 ATTCGTATAGATCGTCCTGTTGTACTGGCAATTAGCGATGAGAGTTTTTATCAAAATGGC 1320

Qy        441 PheLeuAsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIle 460
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Db       1321 TTTTTGAATGAGGACCATTCCTATGATGGGATTCTTGAGTTAGATGCTGGGAAAGACATC 1380

Qy        461 ValIleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGly 480
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Db       1381 GTGATTTCTGCAGATTCTCGCAGTATAGATGCTGTACAATCTCCGTATGGCTATCAGGGA 1440

Qy        481 LysTrpThrIleAsnTrpSerThrAspAspLysLysAlaThrValSerTrpAlaLysGln 500
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Db       1441 AAGTGGACGATCAATTGGTCTACTGATGATAAGAAAGCTACGGTTTCTTGGGCGAAGCAG 1500

Qy        501 SerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySer 520
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Qy        541 GluLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAsn 560
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Db       1621 GAAAAGAGATTTTGGGTTGCAGGCATTTCCAATGTTTTGCATAGGAGCGGTCGTGAAAAT 1680

Qy        561 GlnArgLysPheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArgMetPro 580
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Db       1681 CAAAGGAAATTCCGTCATGTGAGTGGAGGTGCTGTAGTAGGTGCTAGCACGAGGATGCCG 1740

Qy        581 GlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPhe 600
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Db       1741 GGTGGTGATACCTTGTCTCTGGGTTTTGCTCAGCTCTTTGCGCGTGACAAAGACTACTTT 1800

Qy        601 MetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSer 620
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Db       1801 ATGAATACCAATTTCGCAAAGACCTACGCAGGATCTTTACGTTTGCAGCACGATGCTTCC 1860

Qy        621 LeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuPro 640
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Db       1861 CTATACTCTGTGGTGAGTATCCTTTTAGGAGAGGGAGGACTCCGCGAGATCCTGTTGCCT 1920

Qy        641 TyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAsp 660
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Db       1921 TATGTTTCCAAGACTCTGCCGTGCTCTTTCTATGGGCAGCTTAGCTACGGCCATACGGAT 1980

Qy        661 HisArgMetLysThrGluSerLeuProProProProProThrLeuSerThrAspHisThr 680
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Db       1981 CATCGCATGAAGACCGAGTCTCTACCCCCCCCCCCCCCCGACGCTCTCGACGGATCATACT 2040

Qy        681 SerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAlaValGluAsnThr 700
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Db       2041 TCTTGGGGAGGATATGTCTGGGCTGGAGAGCTGGGAACTCGAGTTGCTGTTGAAAATACC 2100

Qy        701 SerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGlnAlaValTyrAla 720
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Db       2101 AGCGGCAGAGGATTTTTCCAAGAGTACACTCCATTTGTAAAAGTCCAAGCTGTTTACGCT 2160

Qy        721 ArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSerAspSerHisLeu 740
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Db       2161 CGCCAAGATAGCTTTGTAGAACTAGGAGCTATCAGTCGTGATTTTAGTGATTCGCATCTT 2220

Qy        741 TyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPheAlaGluGlnTyrTyr 760
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Db       2221 TATAACCTTGCGATTCCTCTTGGAATCAAGTTAGAGAAACGGTTTGCAGAGCAATATTAT 2280

Qy        761 HisValValAlaMetTyrSerProAspValCysArgSerAsnProLysCysThrThrThr 780
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Db       2281 CATGTTGTAGCGATGTATTCTCCAGATGTTTGTCGTAGTAACCCCAAATGTACGACTACC 2340

Qy        781 LeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAlaGly 800
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Db       2341 CTACTTTCCAACCAAGGGAGTTGGAAGACCAAAGGTTCGAACTTAGCAAGACAGGCTGGT 2400

Qy        801 IleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsnPhe 820
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Db       2401 ATTGTTCAGGCCTCAGGTTTTCGATCTTTGGGAGCTGCAGCAGAGCTTTTCGGGAACTTT 2460

Qy        821 GlyPheGluTrpArgGlySerSerArgSerTyrAsnValAspAlaGlySerLysIleLys 840
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Db       2461 GGCTTTGAATGGCGGGGATCTTCTCGTAGCTATAATGTAGATGCGGGTAGCAAAATCAAA 2520

Qy        841 Phe 841
              |||
Db       2521 TTT 2523
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RESULT 2
US-10-289-762-1
; Sequence 1, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
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;   LOCATION: (360001)..(375000)
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Alignment Scores:
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Score:                  4255.00     Matches:        840
Percent Similarity:     99.76%      Conservative:   0
Best Local Similarity:  99.76%      Mismatches:     1
Query Match:            99.07%      Indels:         2
DB:                     12          Gaps:           0

US-09-830-446-27 (1-841) x US-10-289-762-1 (1-1230025)

Qy          1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28950 ATGAAGATTCCACTCCGCTTTTTATTGATATCATTAGTACCTACGCTTTCTATGTCGAAT 29009

Qy         21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29010 TTATTAGGAGCTGCTACTACCGAAGAGTTATCGGCTAGCAATAGCTTCGATGGAACTACA 29069

Qy         41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29070 TCAACAACAAGCTTTTCTAGTAAAACATCATCGGCTACAGATGGCACCAATTATGTTTTT 29129

Qy         61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29130 AAAGATTCTGTAGTTATAGAAAATGTACCCAAAACAGGGGAAACTCAGTCTACTAGTTGT 29189

Qy         81 PheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29190 TTTAAAAATGACGCTGCAGCTGGAGATCTAAATTTCTTAGGAGGGGGATTTTCTTTCACA 29249

Qy        101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29250 TTTAGCAATATCGATGCAACCACGGCTTCTGGAGCTGCTATTGGAAGTGAAGCAGCTAAT 29309

Qy        121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29310 AAGACAGTCACGTTATCAGGATTTTCGGCACTTTCTTTTCTTAAATCCCCAGCAAGTACA 29369

Qy        141 ValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAsp 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29370 GTGACTAATGGATTGGGAGCTATCAATGTTAAAGGGAATTTAAGCCTATTGGATAATGAT 29429

Qy        161 LysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180
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Db      29430 AAGGTATTGATTCAGGACAATTTCTCAACAGGAGATGGCGGACA-ATTAATTGTGCAGGC 29488

Qy        181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArg 200

Db      29489 TCCTTGAAGATCGCAAACAATAAGTCCCTTTCTTTTATTGGAAATAGTTCTTCAACACGT 29548

Qy        201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220

Db      29549 GGCGGAGCGATTCATACCAAAAACCTCACACTATCTTCTGGTGGGGAAACTCTATTTCAG 29608

Qy        221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240

Db      29609 GGGAATACAGCGCCTACGGCTGCTGGTAAAGGAGGTGCTATCGCGATTGCAGACTCTGGC 29668

Qy        241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260

Db      29669 ACCCTATCCATTTCTGGAGACAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCT 29728

Qy        261 ThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeu 280

Db      29729 ACAGGAACCGTCTCTCATAGTGCTATTGATTTAGGAACTAGCGCTAAGATAACTGCGTTA 29788

Qy        281 ArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGlySerThr 300

Db      29789 CGTGCTGCGCAAGGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGACA 29848

Qy        301 SerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGluTyrThr 320

Db      29849 TCTGTTGCTGATGCTCTCAATATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACG 29908

Qy        321 GlyThrIleValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGluLysAsn 340

Db      29909 GGAACCATAGTCTTTTCTGGAGAGAAGCTCACGGAGGCAGAAGCTAAAGATGAGAAGAAC 29968

Qy        341 ArgThrSerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeu-LysGl 360

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Qy        360 yAspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAs 380

Db      30029 TGATGTCGTTTTAAGTGCGAACGGTTTCTCTCAGGATGCAAACTCTAAGTTGATTATGGA 30088

Qy        380 pLeuGlyThrSerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAs 400

Db      30089 TTTAGGGACGTCGTTGGTTGCAAACACCGAAAGTATCGAGTTAACGAATTTGGAAATTAA 30148

Qy        400 nIleAspSerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAs 420

Db      30149 TATAGACTCTCTCAGGAACGGGAAAAAGATAAAACTCAGTGCTGCCACAGCTCAGAAAGA 30208

Qy        420 pIleArgIleAspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGl 440

Db      30209 TATTCGTATAGATCGTCCTGTTGTACTGGCAATTAGCGATGAGAGTTTTTATCAAAATGG 30268

Qy        440 yPheLeuAsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIl 460

Db      30269 CTTTTTGAATGAGGACCATTCCTATGATGGGATTCTTGAGTTAGATGCTGGGAAAGACAT 30328

Qy        460 eValIleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGl 480

Db      30329 CGTGATTTCTGCAGATTCTCGCAGTATAGATGCTGTACAATCTCCGTATGGCTATCAGGG 30388

Qy        480 yLysTrpThrIleAsnTrpSerThrAspAspLysLysAlaThrValSerTrpAlaLysGl 500

Db      30389 AAAGTGGACGATCAATTGGTCTACTGATGATAAGAAAGCTACGGTTTCTTGGGCGAAGCA 30448

Qy        500 nSerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySe 520

Db      30449 GAGTTTTAATCCCACTGCTGAGCAGGAGGCTCCGTTAGTTCCTAATCTTCTTTGGGGTTC 30508

Qy        520 rPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTy 540

Db      30509 TTTTATAGATGTTCGTTCCTTCCAGAATTTTATAGAGCTAGGTACTGAAGGTGCTCCTTA 30568

Qy        540 rGluLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAs 560

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Qy        560 nGlnArgLysPheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArgMetPr 580

Db      30629 TCAAAGGAAATTCCGTCATGTGAGTGGAGGTGCTGTAGTAGGTGCTAGCACGAGGATGCC 30688

Qy        580 oGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPh 600

Db      30689 GGGTGGTGATACCTTGTCTCTGGGTTTTGCTCAGCTCTTTGCGCGTGACAAAGACTACTT 30748

Qy        600 eMetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSe 620

Db      30749 TATGAATACCAATTTCGCAAAGACCTACGCAGGATCTTTACGTTTGCAGCACGATGCTTC 30808

Qy        620 rLeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuPr 640

Db      30809 CCTATACTCTGTGGTGAGTATCCTTTTAGGAGAGGGAGGACTCCGCGAGATCCTGTTGCC 30868

Qy        640 oTyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAs 660

Db      30869 TTATGTTTCCAAGACTCTGCCGTGCTCTTTCTATGGGCAGCTTAGCTACGGCCATACGGA 30928

Qy        660 pHisArgMetLysThrGluSerLeuProProProProProThrLeuSerThrAspHisTh 680

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Qy        680 rSerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAlaValGluAsnTh 700

Db      30989 TTCTTGGGGAGGATATGTCTGGGCTGGAGAGCTGGGAACTCGAGTTGCTGTTGAAAATAC 31048

Qy        700 rSerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGlnAlaValTyrAl 720

Db      31049 CAGCGGCAGAGGATTTTTCCAAGAGTACACTCCATTTGTAAAAGTCCAAGCTGTTTACGC 31108

Qy        720 aArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSerAspSerHisLe 740

Db      31109 TCGCCAAGATAGCTTTGTAGAACTAGGAGCTATCAGTCGTGATTTTAGTGATTCGCATCT 31168

Qy        740 uTyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPheAlaGluGlnTyrTy 760

Db      31169 TTATAACCTTGCGATTCCTCTTGGAATCAAGTTAGAGAAACGGTTTGCAGAGCAATATTA 31228

Qy        760 rHisValValAlaMetTyrSerProAspValCysArgSerAsnProLysCysThrThrTh 780

Db      31229 TCATGTTGTAGCGATGTATTCTCCAGATGTTTGTCGTAGTAACCCCAAATGTACGACTAC 31288

Qy        780 rLeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAlaGl 800

Db      31289 CCTACTTTCCAACCAAGGGAGTTGGAAGACCAAAGGTTCGAACTTAGCAAGACAGGCTGG 31348

Qy        800 yIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsnPh 820

Db      31349 TATTGTTCAGGCCTCAGGTTTTCGATCTTTGGGAGCTGCAGCAGAGCTTTTCGGGAACTT 31408

Qy        820 eGlyPheGluTrpArgGlySerSerArgSerTyrAsnValAspAlaGlySerLysIleLy 840

Db      31409 TGGCTTTGAATGGCGGGGATCTTCTCGTAGCTATAATGTAGATGCGGGTAGCAAAATCAA 31468

Qy        840 sPhe 841

Db      31469 ATTT 31472
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RESULT 3
US-09-428-122-1
; Sequence 1, Application US/09428122
; Publication No. US20030170259A1
; GENERAL INFORMATION:
; APPLICANT: Connaught Laboratories Limited
; APPLICANT: Murdin et al.

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;  TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
;  TITLE OF INVENTION: USES THEREOF
;  FILE REFERENCE: 19721-007-019
;  CURRENT APPLICATION NUMBER: US/09/428,122
;  CURRENT FILING DATE: 1999-10-27
;  EARLIER APPLICATION NUMBER: 60/106,046
;  EARLIER FILING DATE: 1998-10-28
;  EARLIER APPLICATION NUMBER: 60/132,271
;  EARLIER FILING DATE: 1999-05-03
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 3000
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (101)..(2884)
US-09-428-122-1

Alignment Scores:
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Score:                  1580.50        Matches:        375
Percent Similarity:     52.54%         Conservative:   121
Best Local Similarity:  39.72%         Mismatches:     306
Query Match:            36.80%         Indels:         142
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US-09-830-446-27 (1-841) x US-09-428-122-1 (1-3000)

Qy         15 ThrLeuSerMetSerAsnLeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsn 34
Db        134 ACATTTGCTATTTTCCCTTTGTCTATGATTGCTACCGAGACAGTTTTGGATTCAAGTGCG 193

Qy         35 SerPheAspGlyThrThrSerThrThrSerPheSerSerLysThrSerSerAlaThrAsp 54
Db        194 AGTTTCGATGGG---AATAAAAATGGTAATTTTTCAGTTCGTGAGAGTCAGGAAGATGCT 250

Qy         55 GlyThrAsnTyrValPheLysAspSerValValIleGluAsnValProLysThrGlyGlu 74
Db        251 GGAACTACCTACCTATTTAAGGGAAATGTCACTCTAGAAAATATTCCTGGAACAGGCACA 310

Qy         75 ThrGlnSerThrSerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGly 94
Db        311 GCAATCACAAAAAGCTGTTTTAACAAC------ACTAAGGGCGATTTGACTTTCACAGGT 364

Qy         95 GlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIle 114
Db        365 AACGGGAACTCTCTATTGTTCCAAACGGTGGATGCAGGGACTGTAGCAGGGGCTGCTGTT 424

Qy        115 GlySerGluAlaAlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeu 134
Db        425 AACAGCAGCGTGGTAGATAAATCTACCACGTTTATAGGGTTTTCTTCGCTATCTTTTATT 484

Qy        135 LysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValLys---GlyAsn 153
Db        485 GCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGCCGTTAGCTGCTCTACGGGTAGC 544

Qy        154 LeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsnPheSerThrGlyAspGly 173
Db        545 TTGAGTTTGACAAAAAATGTCAGTTTGCTCTTCAGCAAAAACTTTTCAACGGATAATGGC 604

Qy        174 GlyAlaIleAsnCys---------------------------------------------- 178
Db        605 GGTGCTATCACCGCAAAAACTCTTTCATTAACAGGGACTACAATGTCAGCTCTGTTTTCT 664

Qy        178 ---------------------------------------------------------- 178

Db        665 GAAAATACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTACCATTACT 724

Qy        178 ---------------------------------------------------------- 178

Db        725 GGAAACCAAGGGGAAGTCTCTTTTTCTGACAATACTTCTTCGGATTCTGGAGCTGCAATT 784

Qy        179 ------AlaGlySerLeuLysIleAlaAsnAsnLysSerLeuSerPheIle--------- 193
Db        785 TTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTTCCTTTATTGACAATAAG 844

Qy        193 ---------------------------------------------------------- 193

Db        845 GTCACAGGAGCGAGCTCCTCAACAACGGGGGATATGTCAGGAGGTGCTATCTGTGCTTAT 904

Qy        194 ----------------------------------------------------------Gly 194

Db        905 AAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAGCAAC 964

Qy        195 AsnSerSerSerThrArgGlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGly 214
Db        965 AATACATCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTCCGGA 1024

Qy        215 GlyGluThrLeuPhe----------GlnGlyAsnThrAlaProThrAlaAlaGly 229
Db       1025 GGACTTACCCTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCT---------- 1072

Qy        230 LysGlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGly 249
Db       1073 AAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGGT 1132

Qy        250 AspIleIlePheGluGlyAsnThrIleGlyAlaThr------GlyThrValSerHisSer 267
Db       1133 GACATTGTCTTTTTAGGGAATACAGTCACTTCTACTACTCCTGGGACG---AATAGAAGT 1189

Qy        268 AlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyHisThr 287
Db       1190 AGTATCGACTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTGCTGGTAGAGCC 1249

Qy        288 IleTyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsn 307
Db       1250 ATCTACTTCTATGATCCCATAACTACAGGATCATCCACAACAGTTACAGATGTCTTAAAA 1309

Qy        308 IleAsnSerProAspThrGlyAspAsnLysGluTyrThrGlyThrIleValPheSerGly 327
Db       1310 GTTAATGAGACTCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAGGA 1369

Qy        328 GluLysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSerLysLeuLeuGln 347
Db       1370 GAAAAGTTATCAGAGACAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAG 1429

Qy        348 AsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsn 367
Db       1430 CCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAACATGGAGTGACTCTGCAGACTCAG 1489

Qy        368 GlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeu---Val 386
Db       1490 GCATTCACTCAACAGGCAGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAACCT 1549

Qy        387 AlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArgAsn 406
Db       1550 GCTGATACTAGCACCATA------AACAATTTGGTCATTAACATCAGTTCTATAGACGGT 1603

Qy        407 GlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAspArgPro 426
Db       1604 GCAAAGAAGGCAAAAATAGAAACCAAAGCTACGTCAAAAAATCTGACTTTATCTGGAACC 1663

Qy        427 ValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeuAsnGluAspHis 446
Db       1664 ATCACTTTATTGGACCCGACGGGCACGTTTTATGAAAATCATAGTTTAAGAAATCCTCAG 1723

Qy        447 SerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIleSerAla--AspS 466
Db       1724 TCCTACGAC---ATCTTAGAGCTCAAAGCTTCTGGAACTGTAACAAGCACCGCAGTGACT 1780

Qy        466 erArgSerIleAspAlaValGlnSerPro-TyrGlyTyrGlnGlyLysTrp---ThrIle 484
Db       1781 CCAGATCCTATAATGGGTGAGAAATTCCATTACGGCTATCAGGGAACTTGGGGCCCAATT 1840
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Qy       485 AsnTrpSerThrAsp---AspLysLysAlaThrValSerTrpAlaLysGlnSerPheAsn 503
Db      1841 GTTTGGGGGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAAAACTGGCTATATT 1900

Qy       504 ProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySerPheIleAsp 523
Db      1901 CCTAATCCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCATTTATAGAT 1960

Qy       524 ValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTyrGluLysArg 543
Db      1961 ATTAGCTCTCTCCATTATCTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGACCGTGCT 2020

Qy       544 PheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAsnGlnArgLys 563
Db      2021 TTTTGGTGTGCTGGATTATCTAACTTCTTCCATAAGGATAGTACAAAAACACGACGCGGG 2080

Qy       564 PheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArgMetProGlyGlyAsp 583
Db      2081 TTTCGCCATTTGAGTGGCGGTTATGTCATAGGAGGAAACCTACATACTTGTTCAGATAAG 2140

Qy       584 ThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPheMetAsnThr 603
Db      2141 ATTCTTAGTGCTGCATTTTGTCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAG 2200

Qy       604 AsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSerLeuTyrSer 623
Db      2201 AATCAAGGTACAGTCTACGGAGGAACTCTCTATTACCAGCACAACGAAACCTATATCTCT 2260

Qy       624 ValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuProTyrValSer 643
Db      2261 CTTCCTTGC-----------------AAACTACGGCCTTGTTCGTTGTCTTATGTTCCT 2302

Qy       644 LysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAspHisArgMet 663
Db      2303 ACAGAGATTCCTGTTCTCTTTTCAGGAAACCTTAGCTACACCCATACGGATAACGATCTG 2362

Qy       664 LysThrGluSerLeuProProProProProThrLeuSerThrAspHisThrSerTrpGly 683
Db      2363 AAAACCAAGTAT--------------ACAACATATCCTACTGTTAAAGGAAGCTGGGGG 2407

Qy       684 GlyTyrValTrpAlaGlyGluLeuGlyThrArg------ValAlaValGluAsnThrSer 701
Db      2408 AATGATAGTTTCGCTTTAGAATTCGGTGGAAGAGCTCCGATTTGCTTAGATGAAAGTGCT 2467

Qy       702 GlyArgGlyPhePheGlnGluTyrThrProPheValLysValGlnAlaValTyrAlaArg 721
Db      2468 ---------CTATTTGAGCAGTACATGCCCTTCATGAAATTGCAGTTTGTCTATGCACAT 2518

Qy       722 GlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyr 741
Db      2519 CAGGAAGGTTTTAAAGAACAGGGAACAGAAGCTCGTGAATTTGGAAGTAGCCGTCTTGTG 2578

Qy       742 AsnLeuAlaIleProLeuGlyIleLysLeuGluLysArg------PheAlaGluGlnTyr 759
Db      2579 AATCTTGCCTTACCTATCGGGATCCGATTTGATAAGGAATCAGACTGCCAAGATGCAACG 2638

Qy       760 TyrHisValValAlaMetTyrSerProAspValCysArgSerAsnProLysCysThrThr 779
Db      2639 TACAATCTAACTCTTGGTTATACTGTGGATCTTGTTCGTAGTAACCCCGACTGTACGACA 2698

Qy       780 ThrLeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAla 799
Db      2699 ACACTGCGAATTAGCGGTGATTCTTGGAAAACCTTCGGTACGAATTTGGCAAGACAAGCT 2758

Qy       800 GlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsn 819
Db      2759 TTAGTCCTTCGTGCAGGGAACCATTTTTGCTTTAACTCAAATTTTGAAGCCTTTAGCCAA 2818

Qy       820 PheGlyPheGluTrpArgGlySerSerArgSerTyrAsnValAspAlaGlySerLysIle 839
Db      2819 TTTTCTTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTAGACTTAGGAGCAAAATAC 2878

Qy       840 LysPhe 841
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Db      2879 CAATTC 2884

RESULT 4
US-09-738-269-22
; Sequence 22, Application US/09738269
; Publication No. US20030185848A1
; GENERAL INFORMATION:
;  APPLICANT:  JOHNSTON, STEPHEN A.
;  APPLICANT:  STEMKE-HALE, KATHERINE
;  APPLICANT:  SYKES, KATHRYN F.
;  APPLICANT:  KALTENBOECK, BERNHARD
;  TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
;  TITLE OF INVENTION:  NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
;  TITLE OF INVENTION:  CHLAMYDIA PSITTACI
;  FILE REFERENCE:  UTSD:659
;  CURRENT APPLICATION NUMBER: US/09/738,269
;  CURRENT FILING DATE:  2000-12-18
;  NUMBER OF SEQ ID NOS:  61
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 2520
;   TYPE: DNA
;   ORGANISM: Chlamydia psittaci
US-09-738-269-22

Alignment Scores:
Pred. No.:                3.15e-143      Length:          2520
Score:                    1497.00        Matches:         357
Percent Similarity:       56.21%         Conservative:    132
Best Local Similarity:    41.03%         Mismatches:      321
Query Match:              34.85%         Indels:          60
DB:                       13             Gaps:            25

US-09-830-446-27 (1-841) x US-09-738-269-22 (1-2520)

Qy         1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
Db         1 ATGAAACATCCAGTCTACTGGTTCTTAATATCC------TCGAGCCTATTTGCCTCGAAT 54

Qy        21 LeuLeuGlyAlaAlaThrThrGluGlu------LeuSerAlaSerAsnSerPheAspGly 38
Db        55 TCTTTGAGCTTCGCTAACGACGCTCAAACAGCCTTAACTCCCTCCGATAGCTATAATGGA 114

Qy        39 ThrThrSerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyr 58
Db       115 AATGTGACCTCTGAGGAGTTCCAGGTAAAAGAAACTTCATCA------GGAACAACGTAT 168

Qy        59 ValPheLysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThr 78
Db       169 ACTTGTGAAGGCAATGTGTGTATCTCCTTTGCAGGGAAAGATTCAGGTCTAAAGAAA--- 225

Qy        79 SerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSer 98
Db       226 AGTTGTTTC---------TCAGCTACTGATAACCTTACCTTCCTAGGAAACGGGTATACT 276

Qy        99 PheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAla 118
Db       277 CTTTGCTTTGATAATATTACTACTACAGCTAGTAACCCCGGAGCCATTAATGTTCAAGGT 336

Qy       119 AlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAla 138
Db       337 CAAGGAAAAACCTTAGGCATCTCAGGATTTTCTTTATTTTCATGTGCTTATTGTCCTCCA 396

Qy       139 SerThrValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAsp 158
Db       397 GGC------ACAACTGGTTACGGAGCTATACAGACTAAAGGCAACACAACTTTAAAAGAT 450

Qy       159 AsnAspLysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCys 178
Db       451 AACTCTAGTCTTGTCTTCCATAAAAACTGCTCAACAGCAGAAGGTGGGGCTATCCAGTGT 510

Qy       179 AlaGlySer------------LeuLysIleAlaAsnAsnLysSerLeuSerPheIleGly 194
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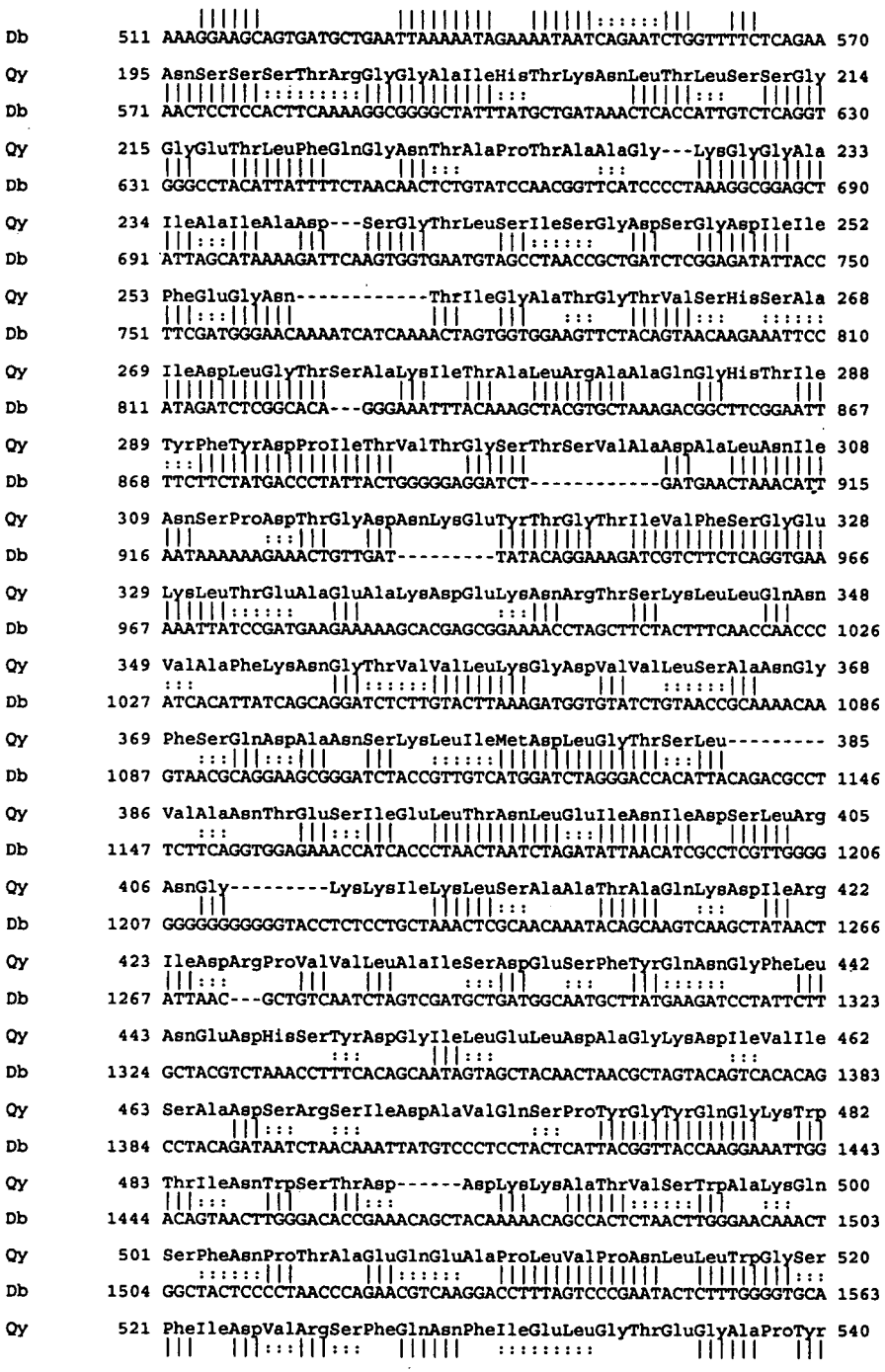

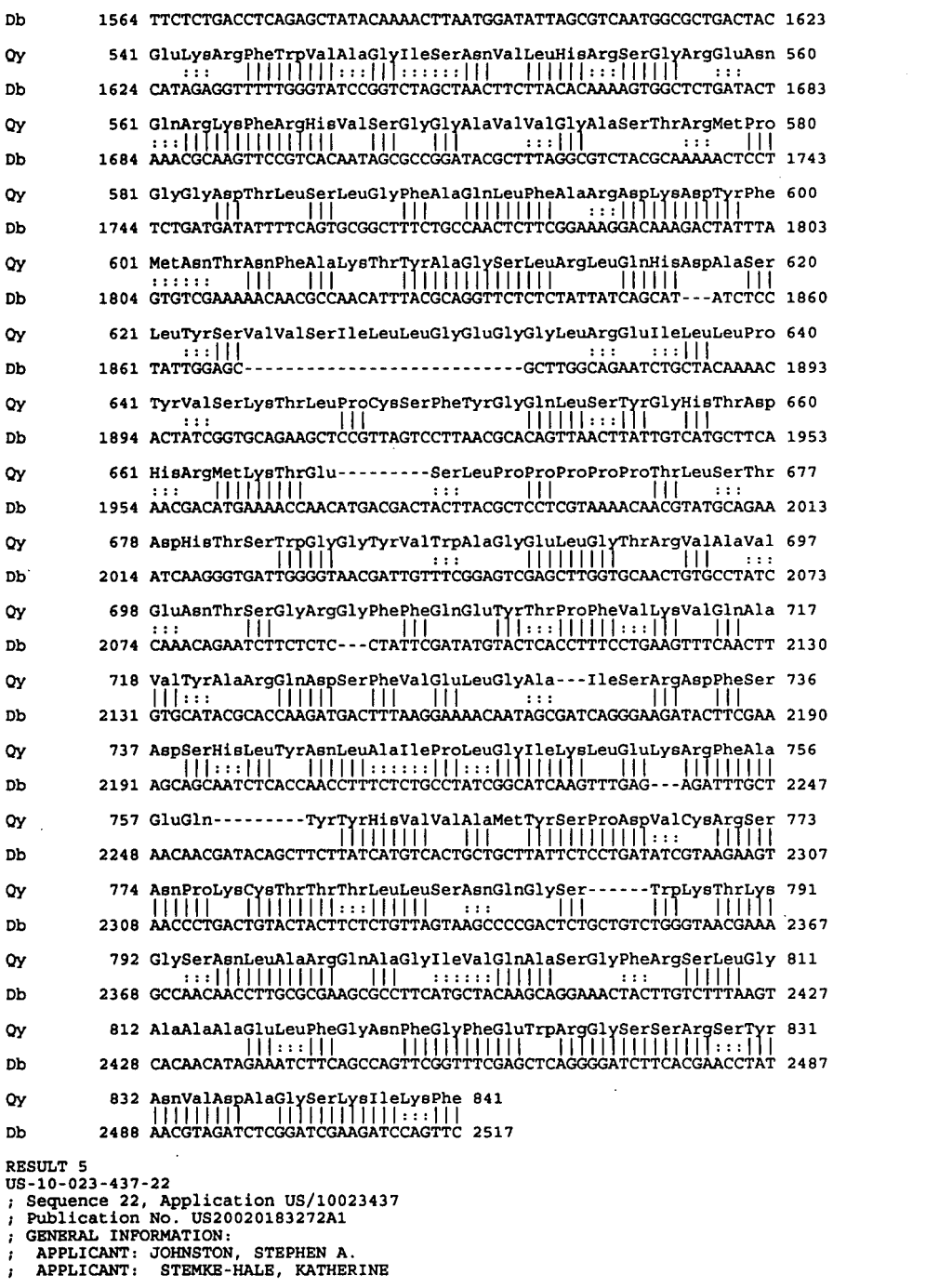

RESULT 5
US-10-023-437-22
; Sequence 22, Application US/10023437
; Publication No. US20020183272A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEMKE-HALE, KATHERINE

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;  APPLICANT:  SYKES, KATHRYN F.
;  APPLICANT:  KALTENBOECK, BERNHARD
;  TITLE OF INVENTION: METHODS AND compositions for Vaccination COMPRISING NUCLEIC ACID
;  TITLE OF INVENTION:  AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
;  FILE REFERENCE: UTSD:736US
;  CURRENT APPLICATION NUMBER: US/10/023,437
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: 60/225,839
;  PRIOR FILING DATE: 2000-12-15
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 2520
;   TYPE: DNA
;   ORGANISM: Chlamydia psittaci
US-10-023-437-22

Alignment Scores:
Pred. No.:                3.15e-143      Length:          2520
Score:                    1497.00        Matches:         357
Percent Similarity:       56.21%         Conservative:    132
Best Local Similarity:    41.03%         Mismatches:      321
Query Match:              34.85%         Indels:          60
DB:                       14             Gaps:            25

US-09-830-446-27 (1-841) x US-10-023-437-22 (1-2520)

Qy          1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
              ||||||   |||:::   :::  |||||||||        :::|||      ||||||
Db          1 ATGAAACATCCAGTCTACTGGTTCTTAATATCC------TCGAGCCTATTTGCCTCGAAT 54

Qy         21 LeuLeuGlyAlaAlaThrThrGluGlu------LeuSerAlaSerAsnSerPheAspGly 38
                 |||      |||          :::      |||:::   |||:::|||::::::|||
Db         55 TCTTTGAGCTTCGCTAACGACGCTCAAACAGCCTTAACTCCCTCCGATAGCTATAATGGA 114

Qy         39 ThrThrSerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyr 58
                 ::::::      |||      |||   :::|||:::      ||||||   |||
Db        115 AATGTGACCTCTGAGGAGTTCCAGGTAAAAGAAACTTCATCA------GGAACAACGTAT 168

Qy         59 ValPheLysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThr 78
                :::   :::|||   |||           |||            :::
Db        169 ACTTGTGAAGGCAATGTGTGTATCTCCTTTGCAGGGAAAGATTCAGGTCTAAAGAAA--- 225

Qy         79 SerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSer 98
              |||||||||          :::|||      :::|||   |||||||||   |||:::::
Db        226 AGTTGTTTC---------TCAGCTACTGATAACCTTACCTTCCTAGGAAACGGGTATACT 276

Qy         99 PheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAla 118
                 |||   ||||||     |||   ::::::      ||||||      :::
Db        277 CTTTGCTTTGATAATATTACTACTACAGCTAGTAACCCCGGAGCCATTAATGTTCAAGGT 336

Qy        119 AlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAla 138
               |||||||:::   :::||||||||||||       |||              |||
Db        337 CAAGGAAAAACCTTAGGCATCTCAGGATTTTCTTTATTTTCATGTGCTTATTGTCCTCCA 396

Qy        139 SerThrValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAsp 158
                 |||   |||   |||||||||       |||||||||   :::|||   |||
Db        397 GGC------ACAACTGGTTACGGAGCTATACAGACTAAAGGCAACACAACTTTAAAAGAT 450

Qy        159 AsnAspLysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCys 178
              |||     ::::::         |||   ||||||   :::||||||||||||   |||
Db        451 AACTCTAGTCTTGTCTTCCATAAAAACTGCTCAACAGCAGAAGGTGGGGCTATCCAGTGT 510

Qy        179 AlaGlySer------------LeuLysIleAlaAsnAsnLysSerLeuSerPheIleGly 194
               |||||||            |||||||||   ||||||::::::|||   |||
Db        511 AAAGGAAGCAGTGATGCTGAATTAAAAATAGAAAATAATCAGAATCTGGTTTTCTCAGAA 570

Qy        195 AsnSerSerSerThrArgGlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGly 214
              |||||||||:::::::::||||||||||||:::         ||||||:::   ||||||
Db        571 AACTCCTCCACTTCAAAAGGCGGGGCTATTTATGCTGATAAACTCACCATTGTCTCAGGT 630

Qy        215 GlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGly---LysGlyGlyAla 233
                 |||   |||||||||       |||:::             :::      ||||||||||||
```

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Db        631 GGGCCTACATTATTTTCTAACAACTCTGTATCCAACGGTTCATCCCCTAAAGGCGGAGCT 690

Qy        234 IleAlaIleAlaAsp---SerGlyThrLeuSerIleSerGlyAspSerGlyAspIleIle 252
                |||:::|||   |||   ||||||       |||::::::   |||   |||||||||
Db        691 ATTAGCATAAAAGATTCAAGTGGTGAATGTAGCCTAACCGCTGATCTCGGAGATATTACC 750

Qy        253 PheGluGlyAsn------------ThrIleGlyAlaThrGlyThrValSerHisSerAla 268
                |||:::||||||            |||   |||   :::   ||||||:::   ::::::
Db        751 TTCGATGGGAACAAAATCATCAAAACTAGTGGTGGAAGTTCTACAGTAACAAGAAATTCC 810

Qy        269 IleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyHisThrIle 288
              ||||||||||||||       |||   |||   |||||||||       |||       |||
Db        811 ATAGATCTCGGCACA---GGGAAATTTACAAAGCTACGTGCTAAAGACGGCTTCGGAATT 867

Qy        289 TyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsnIle 308
                :::|||||||||||||||||      ||||||            |||   |||||||||
Db        868 TTCTTCTATGACCCTATTACTGGGGGAGGATCT------------GATGAACTAAACATT 915

Qy        309 AsnSerProAspThrGlyAspAsnLysGluTyrThrGlyThrIleValPheSerGlyGlu 328
                |||       :::|||   |||          |||||||||   ||||||||||||||||||
Db        916 AATAAAAAAGAAACTGTTGAT---------TATACAGGAAAGATCGTCTTCTCAGGTGAA 966

Qy        329 LysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSerLysLeuLeuGlnAsn 348
                ||||||::::::   |||            :::|||       |||          |||
Db        967 AAATTATCCGATGAAGAAAAAGCACGAGCGGAAAACCTAGCTTCTACTTTCAACCAACCC 1026

Qy        349 ValAlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsnGly 368
                :::          |||::::::|||||||||       |||   ::::::|||
Db       1027 ATCACATTATCAGCAGGATCTCTTGTACTTAAAGATGGTGTATCTGTAACCGCAAAACAA 1086

Qy        369 PheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeu--------- 385
                :::|||:::|||   |||   ::::::||||||||||||:::|||
Db       1087 GTAACGCAGGAAGCGGGATCTACCGTTGTCATGGATCTAGGGACCACATTACAGACGCCT 1146

Qy        386 ValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArg 405
                :::      |||:::|||   ||||||||||||:::|||||||||   ||||||
Db       1147 TCTTCAGGTGGAGAAACCATCACCCTAACTAATCTAGATATTAACATCGCCTCGTTGGGG 1206

Qy        406 AsnGly---------LysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArg 422
                |||              ||||||:::      ||||||   :::   |||
Db       1207 GGGGGGGGGGGTACCTCTCCTGCTAAACTCGCAACAAATACAGCAAGTCAAGCTATAACT 1266

Qy        423 IleAspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeu 442
                |||:::      |||   |||      :::|||   :::   |||::::::      |||
Db       1267 ATTAAC---GCTGTCAATCTAGTCGATGCTGATGGCAATGCTTATGAAGATCCTATTCTT 1323

Qy        443 AsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIle 462
                        :::      |||:::                        :::
Db       1324 GCTACGTCTAAACCTTTCACAGCAATAGTAGCTACAACTAACGCTAGTACAGTCACACAG 1383

Qy        463 SerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGlyLysTrp 482
                  |||:::   :::                  :::   ||||||||||||||   |||
Db       1384 CCTACAGATAATCTAACAAATTATGTCCCTCCTACTCATTACGGTTACCAAGGAAATTGG 1443

Qy        483 ThrIleAsnTrpSerThrAsp------AspLysLysAlaThrValSerTrpAlaLysGln 500
                |||:::   |||   |||:::         |||   ||||||::::::|||   :::
Db       1444 ACAGTAACTTGGGACACCGAAACAGCTACAAAAACAGCCACTCTAACTTGGGAACAAACT 1503

Qy        501 SerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySer 520
                :::::::|||       |||::::::   |||||||||||||||   |||||||:::
Db       1504 GGCTACTCCCCTAACCCAGAACGTCAAGGACCTTTAGTCCCGAATACTCTTTGGGGTGCA 1563

Qy        521 PheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTyr 540
                |||   |||:::|||:::   ||||||   :::::::::         ||||||   |||
Db       1564 TTCTCTGACCTCAGAGCTATACAAAACTTAATGGATATTAGCGTCAATGGCGCTGACTAC 1623

Qy        541 GluLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAsn 560
                :::   ||||||||||:::|||::::::|||   ||||||:::|||||||   :::
Db       1624 CATAGAGGTTTTTGGGTATCCGGTCTAGCTAACTTCTTACACAAAAGTGGCTCTGATACT 1683

Qy        561 GlnArgLysPheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArgMetPro 580
                :::|||||||||||||||   |||   |||      :::|||         :::   |||
Db       1684 AAACGCAAGTTCCGTCACAATAGCGCCGGATACGCTTTAGGCGTCTACGCAAAAACTCCT 1743
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Qy        581 GlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPhe 600
Db       1744 TCTGATGATATTTTCAGTGCGGCTTTCTGCCAACTCTTCGGAAAGGACAAAGACTATTTA 1803

Qy        601 MetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSer 620
Db       1804 GTGTCGAAAAACAACGCCAACATTTACGCAGGTTCTCTCTATTATCAGCAT---ATCTCC 1860

Qy        621 LeuTyrSerValValSerIleLeuGluGlyGlyLeuArgGluIleLeuLeuPro 640
Db       1861 TATTGGAGC-------------------------GCTTGGCAGAATCTGCTACAAAAC 1893

Qy        641 TyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAsp 660
Db       1894 ACTATCGGTGCAGAAGCTCCGTTAGTCCTTAACGCACAGTTAACTTATTGTCATGCTTCA 1953

Qy        661 HisArgMetLysThrGlu---------SerLeuProProProProProThrLeuSerThr 677
Db       1954 AACGACATGAAAACCAACATGACGACTACTTACGCTCCTCGTAAAACAACGTATGCAGAA 2013

Qy        678 AspHisThrSerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAlaVal 697
Db       2014 ATCAAGGGTGATTGGGGTAACGATTGTTTCGGAGTCGAGCTTGGTGCAACTGTGCCTATC 2073

Qy        698 GluAsnThrSerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGlnAla 717
Db       2074 CAAACAGAATCTTCTCTC---CTATTCGATATGTACTCACCTTTCCTGAAGTTTCAACTT 2130

Qy        718 ValTyrAlaArgGlnAspSerPheValGluLeuGlyAla---IleSerArgAspPheSer 736
Db       2131 GTGCATACGCACCAAGATGACTTTAAGGAAAACAATAGCGATCAGGGAAGATACTTCGAA 2190

Qy        737 AspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPheAla 756
Db       2191 AGCAGCAATCTCACCAACCTTTCTCTGCCTATCGGCATCAAGTTTGAG---AGATTTGCT 2247

Qy        757 GluGln---------TyrTyrHisValValAlaMetTyrSerProAspValCysArgSer 773
Db       2248 AACAACGATACAGCTTCTTATCATGTCACTGCTGCTTATTCTCCTGATATCGTAAGAAGT 2307

Qy        774 AsnProLysCysThrThrThrLeuLeuSerAsnGlnGlySer------TrpLysThrLys 791
Db       2308 AACCCTGACTGTACTACTTCTCTGTTAGTAAGCCCCGACTCTGCTGTCTGGGTAACGAAA 2367

Qy        792 GlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGly 811
Db       2368 GCCAACAACCTTGCGCGAAGCGCCTTCATGCTACAAGCAGGAAACTACTTGTCTTTAAGT 2427

Qy        812 AlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArgSerTyr 831
Db       2428 CACAACATAGAAATCTTCAGCCAGTTCGGTTTCGAGCTCAGGGGATCTTCACGAACCTAT 2487

Qy        832 AsnValAspAlaGlySerLysIleLysPhe 841
Db       2488 AACGTAGATCTCGGATCGAAGATCCAGTTC 2517

RESULT 6
US-10-312-273-116
; Sequence 116, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
;  FILE REFERENCE: P025035WO
;  CURRENT APPLICATION NUMBER: US/10/312,273
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: 0016363.4
;  PRIOR FILING DATE: 2000-07-03
;  PRIOR APPLICATION NUMBER: 0017047.2
;  PRIOR FILING DATE: 2000-07-11
;  PRIOR APPLICATION NUMBER: 0017983.8
;  PRIOR FILING DATE: 2000-07-21
;  PRIOR APPLICATION NUMBER: 0019368.0
;  PRIOR FILING DATE: 2000-08-07
;  PRIOR APPLICATION NUMBER: 0020440.4
;  PRIOR FILING DATE: 2000-08-18
;  PRIOR APPLICATION NUMBER: 0022583.9
;  PRIOR FILING DATE: 2000-09-14
;  PRIOR APPLICATION NUMBER: 0027549.5
;  PRIOR FILING DATE: 2000-11-10
;  PRIOR APPLICATION NUMBER: 0031706.5
;  PRIOR FILING DATE: 2000-12-22
;  NUMBER OF SEQ ID NOS: 664
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 116
;   LENGTH: 2787
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-312-273-116

Alignment Scores:
Pred. No.:                7.71e-137      Length:          2787
Score:                    1435.50        Matches:         340
Percent Similarity:       51.43%         Conservative:    147
Best Local Similarity:    35.90%         Mismatches:      335
Query Match:              33.42%         Indels:          125
DB:                       12             Gaps:            15

US-09-830-446-27 (1-841) x US-10-312-273-116 (1-2787)

Qy          1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
Db          1 ATGAAGACTTCGATTCCTTGGGTTTTAGTTTCCTCCGTGTTAGCTTTCTCA---TGTCAC 57

Qy         21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
Db         58 CTACAGTCACTAGCTAACGAGGAACTTTTATCACCTGATGATAGCTTTAATGGAAATATC 117

Qy         41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
Db        118 GATTCAGGAACGTTTACTCCAAAAACTTCAGCC-----------ACAACATATTCTCTA 165

Qy         61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCys 80
Db        166 ACAGGAGATGTCTTCTTTTACGAG---CCTGGAAAAGGCACTCCCTTATCTGACAGTTGT 222

Qy         81 PheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr 100
Db        223 TTTAAGCAA------ACCACGGACAATCTTACCTTCTTGGGGAACGGTCATAGCTTAACG 276

Qy        101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsn 120
Db        277 TTTGGCTTTATAGATGCTGGCACTCATGCAGGTGCTGCT---GCATCTACAACAGCAAAT 333

Qy        121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
Db        334 AAGAATCTTACCTTCTCAGGGTTTTCCTTACTGAGTTTTGATTCCTCTCCTAGCACAACG 393

Qy        141 ValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAsp 160
Db        394 GTTACTACAGGTCAGGGAACGCTTTCCTCAGCAGGAGGCGTAAATTTAGAAAATATTCGT 453

Qy        161 LysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180
Db        454 AAACTTGTAGTTGCTGGGAATTTTTCTACTGCAGATGGTGGAGCTATCAAAGGAGCGTCT 513

Qy        180 ------------------------------------------------------------ 180
Db        514 TTCCTTTTAACTGGCACTTCTGGAGATGCTCTTTTTAGTAACAACTCTTCATCAACAAAG 573

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Qy        180 ------------------------------------------------------------ 180
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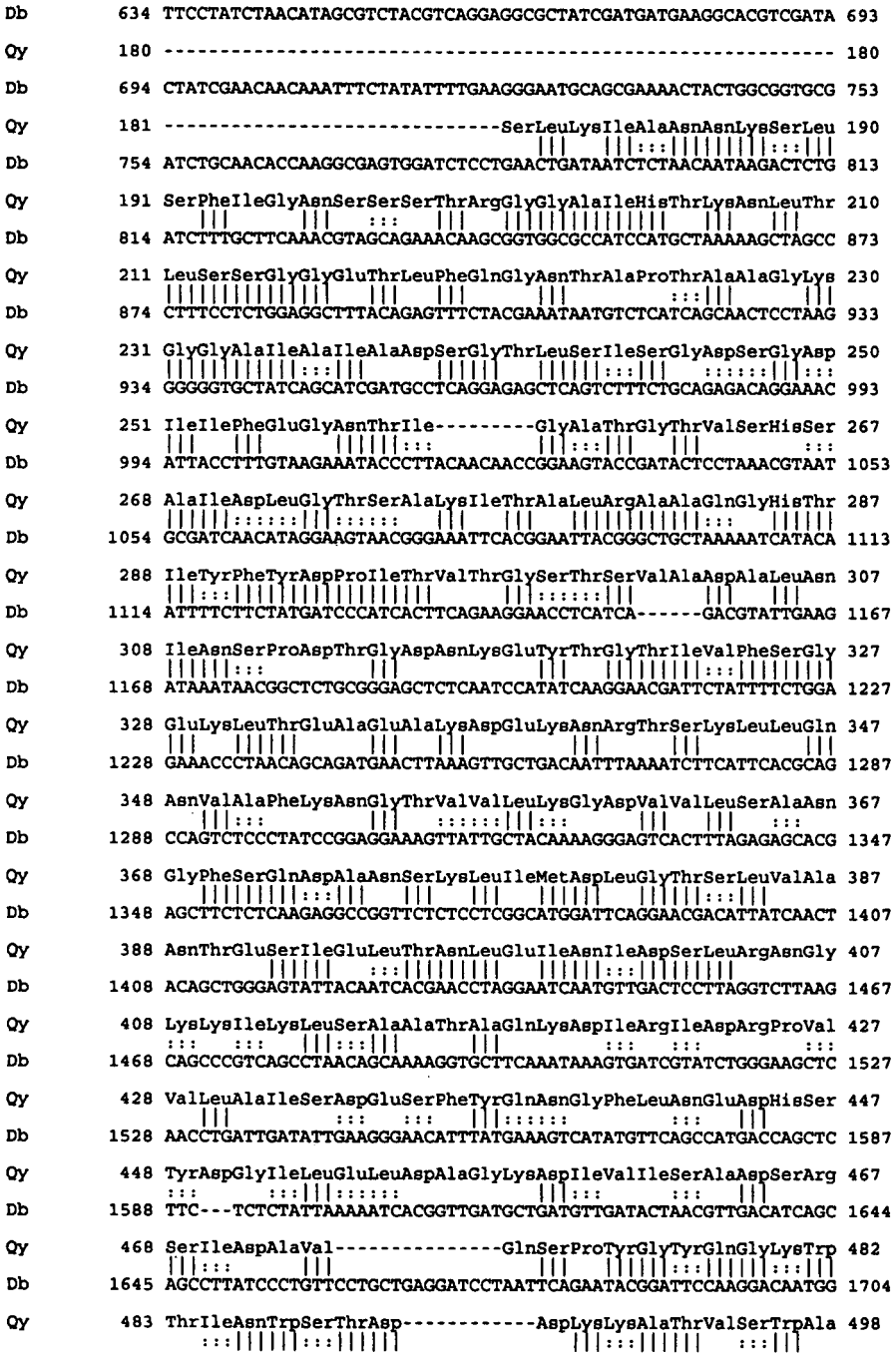
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Db 754 ATCTGCAACACCAAGGCGAGTGGATCTCCTGAACTGATAATCTCTAACAATAAGACTCTG 813
Qy 191 SerPheIleGlyAsnSerSerSerThrArgGlyGlyAlaIleHisThrLysAsnLeuThr 210
Db 814 ATCTTTGCTTCAAACGTAGCAGAAACAAGCGGTGGCGCCATCCATGCTAAAAAGCTAGCC 873
Qy 211 LeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGlyLys 230
Db 874 CTTTCCTCTGGAGGCTTTACAGAGTTTCTACGAAATAATGTCTCATCAGCAACTCCTAAG 933
Qy 231 GlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGlyAsp 250
Db 934 GGGGGTGCTATCAGCATCGATGCCTCAGGAGAGCTCAGTCTTTCTGCAGAGACAGGAAAC 993
Qy 251 IleIlePheGluGlyAsnThrIle---------GlyAlaThrGlyThrValSerHisSer 267
Db 994 ATTACCTTTGTAAGAAATACCCTTACAACAACCGGAAGTACCGATACTCCTAAACGTAAT 1053
Qy 268 AlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyHisThr 287
Db 1054 GCGATCAACATAGGAAGTAACGGGAAATTCACGGAATTACGGGCTGCTAAAAATCATACA 1113
Qy 288 IleTyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsn 307
Db 1114 ATTTTCTTCTATGATCCCATCACTTCAGAAGGAACCTCATCA------GACGTATTGAAG 1167
Qy 308 IleAsnSerProAspThrGlyAspAsnLysGluTyrThrGlyThrIleValPheSerGly 327
Db 1168 ATAAATAACGGCTCTGCGGGAGCTCTCAATCCATATCAAGGAACGATTCTATTTTCTGGA 1227
Qy 328 GluLysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSerLysLeuGln 347
Db 1228 GAAACCCTAACAGCAGATGAACTTAAAGTTGCTGACAATTTAAAATCTTCATTCACGCAG 1287
Qy 348 AsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsn 367
Db 1288 CCAGTCTCCCTATCCGGAGGAAAGTTATTGCTACAAAAGGGAGTCACTTTAGAGAGCACG 1347
Qy 368 GlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeuValAla 387
Db 1348 AGCTTCTCTCAAGAGGCCGGTTCTCTCCTCGGCATGGATTCAGGAACGACATTATCAACT 1407
Qy 388 AsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArgAsnGly 407
Db 1408 ACAGCTGGGAGTATTACAATCACGAACCTAGGAATCAATGTTGACTCCTTAGGTCTTAAG 1467
Qy 408 LysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAspArgProVal 427
Db 1468 CAGCCCGTCAGCCTAACAGCAAAAGGTGCTTCAAATAAAGTGATCGTATCTGGGAAGCTC 1527
Qy 428 ValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeuAsnGluAspHisSer 447
Db 1528 AACCTGATTGATATTGAAGGGAACATTTATGAAAGTCATATGTTCAGCCATGACCAGCTC 1587
Qy 448 TyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIleSerAlaAspSerArg 467
Db 1588 TTC---TCTCTATTAAAAATCACGGTTGATGCTGATGTTGATACTAACGTTGACATCAGC 1644
Qy 468 SerIleAspAlaVal---------------GlnSerProTyrGlyTyrGlnGlyLysTrp 482
Db 1645 AGCCTTATCCCTGTTCCTGCTGAGGATCCTAATTCAGAATACGGATTCCAAGGACAATGG 1704
Qy 483 ThrIleAsnTrpSerThrAsp------------AspLysLysAlaThrValSerTrpAla 498
Db 1705 AATGTTAATTGGACTACGGATACAGCTACAAATACAAAAGAGGCCACGGCAACTTGGACC 1764
Qy 499 LysGlnSerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrp 518
Db 1765 AAAACAGGATTTGTTCCCAGCCCCGAAAGAAAATCTGCGTTAGTATGCAATACCCTATGG 1824
Qy 519 GlySerPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAla 538
Db 1825 GGAGTCTTTACTGACATTCGCTCTCTGCAACAGCTTGTAGAGATCGGCGCAACTGGTATG 1884
Qy 539 ProTyrGluLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArg 558
Db 1885 GAACACAAACAAGGTTTCTGGGTTTCCTCCATGACGAACTTCCTGCATAAGACTGGAGAT 1944
Qy 559 GluAsnGlnArgLysPheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArg 578
Db 1945 GAAAATCGCAAAGGCTTCCGTCATACCTCTGGAGGCTACGTCATCGGTGGAAGTGCTCAC 2004
Qy 579 MetProGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAsp 598
Db 2005 ACTCCTAAAGACGACCTATTTACCTTTGCGTTCTGCCATCTCTTTGCTAGAGACAAAGAT 2064
Qy 599 TyrPheMetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAsp 618
Db 2065 TGTTTTATCGCTCACAACAACTCTAGAACCTACGGTGGAACTTTATTCTTCAAGCACTCT 2124
Qy 619 AlaSerLeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeu 638
Db 2125 CATACCCTACAACCCCAAAACTATTTGAGATTAGGAAGAGCAAAGTTTTCTGAATCAGCT 2184
Qy 639 LeuProTyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHis 658
Db 2185 ATAGAAAAATTCCCTAGGGAAATTCCCCTAGCCTTGGATGTCCAAGTTTCGTTCAGCCAT 2244
Qy 659 ThrAspHisArgMetLysThrGlu------SerLeuProProProProProThrLeuSer 676
Db 2245 TCAGACAACCGTATGGAAACGCACTATACCTCATTGCCA---------- 2283
Qy 677 ThrAspHisThrSerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAla 696
Db 2284 GAATCCGAAGGTTCTTGGAGCAACGAGTGTATAGCTGGTGGTATCGGCCTAGACCTTCCT 2343
Qy 697 ValGluAsnThrSerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGln 716
Db 2344 TTTGTTCTTTCCAACCCACATCCTCTTTTCAAGACCTTCATTCCACAGATGAAAGTCGAA 2403
Qy 717 AlaValTyrAlaArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSer 736
Db 2404 ATGGTTTATGTATCACAAAATAGCTTCTTCGAAAGCTCTAGTGATGGCCGTGGTTTTAGT 2463
Qy 737 AspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLys---LeuGluLysArgPhe 755
Db 2464 ATTGGAAGGCTGCTTAACCTCTCGATTCCTGTGGGTGCGAAATTCGTGCAGGGGGATATC 2523
Qy 756 AlaGluGlnTyr---TyrHisValValAlaMetTyrSerProAspValCysArgSerAsn 774
Db 2524 GGAGATTCCTACACCTATGATCTCTCAGGATTCTTTGTTTCCGATGTCTATCGTAACAAT 2583
Qy 775 ProLysCysThrThrThrLeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsn 794
Db 2584 CCCCAATCTACAGCGACTCTTGTGATGAGCCCAGACTCTTGGAAAATTCGCGGTGGCAAT 2643
Qy 795 LeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAla 814
Db 2644 CTTTCAAGACAGGCATTTTTACTGAGGGGTAGCAACAACTACGTCTACAACTCCAATTGT 2703
Qy 815 GluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArgSerTyrAsnValAsp 834
Db 2704 GAGCTCTTCGGACATTACGCTATGGAACTCCGTGGATCTTCAAGGAACTACAATGTAGAT 2763
Qy 835 AlaGlySerLysIleLysPhe 841
Db 2764 GTTGGTACCAAACTCCGATTC 2784

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RESULT 7
US-10-312-273-46
; Sequence 46, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
;  FILE REFERENCE: P025035WO
;  CURRENT APPLICATION NUMBER: US/10/312,273
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: 0016363.4
;  PRIOR FILING DATE: 2000-07-03
;  PRIOR APPLICATION NUMBER: 0017047.2
;  PRIOR FILING DATE: 2000-07-11
;  PRIOR APPLICATION NUMBER: 0017983.8
;  PRIOR FILING DATE: 2000-07-21
;  PRIOR APPLICATION NUMBER: 0019368.0
;  PRIOR FILING DATE: 2000-08-07
;  PRIOR APPLICATION NUMBER: 0020440.4
;  PRIOR FILING DATE: 2000-08-18
;  PRIOR APPLICATION NUMBER: 0022583.9
;  PRIOR FILING DATE: 2000-09-14
;  PRIOR APPLICATION NUMBER: 0027549.5
;  PRIOR FILING DATE: 2000-11-10
;  PRIOR APPLICATION NUMBER: 0031706.5
;  PRIOR FILING DATE: 2000-12-22
;  NUMBER OF SEQ ID NOS: 664
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 46
;   LENGTH: 2793
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-312-273-46

Alignment Scores:
Pred. No.:              8.79e-135       Length:         2793
Score:                  1415.50         Matches:        352
Percent Similarity:     50.53%          Conservative:   129
Best Local Similarity:  36.97%          Mismatches:     338
Query Match:            32.96%          Indels:         133
DB:                     12              Gaps:           19

US-09-830-446-27 (1-841) x US-10-312-273-46 (1-2793)

Qy          1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
              ||||||||||||||||      ||||||||||||      ||||||
Db          1 ATGAAAATACCCTTGCACAAACTCCTGATCTCT------TCGACTCTTGTCACTCCCATT 54

Qy         21 LeuLeuGlyAlaAlaThr---------ThrGluGluLeuSerAlaSerAsnSerPheAsp 37
              ||||||      ||||||                    ||||||   ::::::|||||||||
Db         55 CTATTGAGCATTGCAACTTACGGAGCAGATGCTTCTTTATCCCCTACAGATAGCTTTGAT 114

Qy         38 GlyThrThrSerThrThrSerPheSerSerLysThrSérSerAlaThrAspGlyThrAsn 57
              |||         :::|||   |||:::   |||::::::::::     :::||||||||||
Db        115 GGAGCGGGCGGCTCTACA---TTTACTCCAAAATCTACAGCAGATGCCAATGGAACGAAC 171

Qy         58 TyrValPheLysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSer 77
              ||||||          :::|||   |||   :::       |||   |||          :::
Db        172 TATGTCTTATCAGGAAATGTCTATATAAACGATGCTGGGAAA---GGCACAGCATTAACA 228

Qy         78 ThrSerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPhe 97
                 ||||||                    |||||||||   |||   |||   |||:::
Db        229 GGCTGCTGCTTTACAGAA------ACTACGGGTGATCTGACATTTACTGGAAAGGGATAC 282

Qy         98 SerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGlu 117
              ||||||:::|||:::   :::||||||   :::   :::|||||||||     |||
Db        283 TCATTTTCATTCAACACGGTAGATGCGGGTTCGAATGCAGGAGCTGCG---GCAAGCACA 339

Qy        118 AlaAlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerPro 137
                 |||:::|||   :::|||   :::||||||||||   |||||||||:::   :::|||
Db        340 ACTGCTGATAAAGCCCTAACATTCACAGGATTTTCTAACCTTTCCTTCATTGCAGCTCCT 399

Qy        138 AlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeu 157
                 :::||||||   :::|||          ::::::      |||   |||:::|||
Db        400 GGAACTACAGTTGCTTCAGGAAAAAGTACTTTAAGTTCTGCAGGAGCCTTAAATCTTACC 459

Qy        158 AspAsnAspLysValLeuIleGlnAspAsnPheSer---------------------- 169
              ||||||     :::|||          |||   |||
Db        460 GATAATGGAACGATTCTCTTTAGCCAAAACGTCTCCAATGAAGCTAATAACAATGGCGGA 519

Qy        169 ---------------------------------------------------------- 169

Db        520 GCGATCACCACAAAAACTCTTTCTATTTCTGGGAATACCTCTTCTATAACCTTCACTAGT 579

Qy        169 ---------------------------------------------------------- 169

Db        580 AATAGCGCAAAAAAATTAGGTGGAGCGATCTATAGCTCTGCGGCTGCAAGTATTTCAGGA 639

Qy        169 ---------------------------------------------------------- 169

Db        640 AACACCGGCCAGTTAGTCTTTATGAATAATAAAGGAGAAACTGGGGGTGGGGCTCTGGGC 699

Qy        169 ---------------------------------------------------------- 169

Db        700 TTTGAAGCCAGCTCCTCGATTACTCAAAATAGCTCCCTTTTCTTCTCTGGAAACACTGCA 759

Qy        170 ---------ThrGlyAspGlyGlyAlaIleAsnCys---------------AlaGlySer 181
                        |||   ||||||||||||   |||                  :::
Db        760 ACAGATGCTGCAGGCAAGGGCGGGGCCATTTATTGTGAAAAAACAGGAGAGACTCCTACT 819

Qy        182 LeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArgGly 201
              |||   |||:::   |||||||||||||:::|||       |||||||||   |||:::|||
Db        820 CTTACTATCTCTGGAAATAAAAGTCTGACCTTCGCCGAGAACTCTTCAGTAACTCAAGGC 879

Qy        202 GlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGly 221
              ||||||||          |||   ||||||:::   |||   |||||||||
Db        880 GGAGCAATCTGTGCCCATGGTCTAGATCTTTCCGCTGCTGGCCCTACCCTATTTTCAAAT 939

Qy        222 Asn---ThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        940 AATAGATGCGGGAACACAGCTGCAGGCAAGGGCGGCGCTATTGCAATTGCCGACTCTGGA 999

Qy        241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260
              :::|||||:::|||   :::   |||||||||   |||   |||||||||:::   :::
Db       1000 TCTTTAAGTCTCTCTGCAAATCAAGGAGACATCACGTTCCTTGGCAACACTCTAACCTCA 1059

Qy        261 ThrGly------ThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThr 278
              |||         |||   :::   :::||||||   ||||||:::|||||||||||||||
Db       1060 ACCTCCGCGCCAACATCGACACGGAATGCTATCTACCTGGGATCGTCAGCAAAAATTACG 1119

Qy        279 AlaLeuArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGly 298
              ||||||||||||||||||   :::||||||||||||||||||||||      :::
Db       1120 AACTTAAGGGCAGCCCAAGGCCAATCTATCTATTTCTATGATCCGATT---GCATCTAAC 1176

Qy        299 SerThrSerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGlu 318
              :::|||      :::|||   |||   ||||||   ||||||:::            :::
Db       1177 ACCACAGGAGCTTCAGACGTTCTGACCATCAACCAACCGGATAGCAACTCGCCTTTAGAT 1236

Qy        319 TyrThrGlyThrIleValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGlu 338
              |||:::||||||||||||||||||||||||||||||:::      |||||||||
Db       1237 TATTCAGGAACGATTGTATTTTCTGGGGAAAAGCTCTCTGCAGATGAAGCGAAAGCTGCT 1296

Qy        339 LysAsnArgThrSerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeu 358
              |||   ||||||   |||   |||   :::|||      :::|||||:::   |||
Db       1297 GATAACTTCACATCTATATTAAAGCAACCATTGGCTCTAGCCTCTGGAACCTTAGCACTC 1356

Qy        359 LysGlyAspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIle 378
              ||||||:::|||   |||       |||||||||:::|||          |||   |||:::
Db       1357 AAAGGAAATGTCGAGTTAGATGTCAATGGTTTCACACAGACTGAAGGCTCTACACTCCTC 1416

Qy        379 MetAspLeuGlyThrSerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGlu 398
              |||       ||||||   |||   |||:::|||||||:::|||   ||||||   |||
Db       1417 ATGCAACCAGGAACAAAGCTCAAAGCAGATACTGAAGCTATCAGTCTTACCAAACTTGTC 1476

Qy        399 IleAsnIleAspSerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGln 418
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Db       1477 GTTGATCTTTCTGCCTTAGAGGGAAATAAGAGTGTGTCCATTGAAACAGCAGGAGCCAAC 1536

Qy        419 LysAspIleArgIleAspArgProValValLeuAlaIleSerAspGluSerPheTyrGln 438

Db       1537 AAAACTATAACTCTAACCTCTCCTCTTGTTTTCCAAGATAGTAGCGGCAATTTTTATGAA 1596

Qy        439 AsnGlyPheLeuAsnGluAspHisSerTyrAspGlyIleLeu------GluLeuAspAla 456

Db       1597 AGCCATACGATAAACCAAGCCTTCACGCAGCCTTTGGTGGTATTCACTGCTGCTACTGCT 1656

Qy        457 GlyLysAspIleValIleSerAlaAspSerArgSerIleAspAlaValGlnSerPro--- 475

Db       1657 GCTAGCGATATTTATATC------GATGCGCTTCTCACTTCTCCAGTACAAACTCCAGAA 1710

Qy        476 ------TyrGlyTyrGlnGlyLysTrpThrIleAsnTrp------SerThrAspAspLys 491

Db       1711 CCTCATTACGGGTATCAGGGACATTGGGAAGCCACTTGGGCAGACACATCAACTGCAAAA 1770

Qy        492 LysAlaThrValSerTrpAlaLysGlnSerPheAsnProThrAlaGluGlnGluAlaPro 511

Db       1771 TCAGGAACTATGACTTGGGTAACTACGGGCTACAACCCTAATCCTGAGCGTAGAGCTTCC 1830

Qy        512 LeuValProAsnLeuLeuTrpGlySerPheIleAspValArgSerPheGlnAsnPheIle 531

Db       1831 GTAGTTCCCGATTCATTATGGGCATCCTTTACTGACATTCGCACTCTACAGCAGATCATG 1890

Qy        532 GluLeuGlyThrGluGlyAlaProTyrGluLysArgPheTrpValAlaGlyIleSerAsn 551

Db       1891 ACATCTCAAGCGAATAGTATCTATCAGCAACGAGGACTCTGGGCATCAGGAACTGCGAAT 1950

Qy        552 ValLeuHisArgSerGlyArgGluAsnGlnArgLysPheArgHisValSerGlyGlyAla 571

Db       1951 TTCTTCCATAAGGATAAATCAGGAACTAACCAAGCATTCCGACATAAAAGCTACGGCTAT 2010

Qy        572 ValValGlyAlaSerThrArgMetProGlyGlyAspThrLeuSerLeuGlyPheAlaGln 591

Db       2011 ATTGTTGGAGGAAGTGCTGAAGATTTTTCTGAAAATATCTTCAGTGTAGCTTTCTGCCAG 2070

Qy        592 LeuPheAlaArgAspLysAspTyrPheMetAsnThrAsnPheAlaLysThrTyrAlaGly 611

Db       2071 CTCTTCGGTAAAGATAAAGACCTGTTTATAGTTGAAAATACCTCTCATAACTATTTAGCG 2130

Qy        612 SerLeuArgLeuGlnHisAspAlaSerLeuTyrSerValValSerIleLeuLeuGlyGlu 631

Db       2131 TCGCTATACCTGCAACATCGAGCATTCCTAGGAGGACTTCCC------ATGCCCTCATTT 2184

Qy        632 GlyGlyLeuArgGluIleLeuLeuProTyrValSerLysThrLeuProCysSerPheTyr 651

Db       2185 GGAAGTATCACCGACATGCTG--------------AAAGATATTCCTCTCATTTTGAAT 2229

Qy        652 GlyGlnLeuSerTyrGlyHisThrAspHisArgMetLysThrGluSerLeuProProPro 671

Db       2230 GCCCAGCTAAGCTACAGCTACACTAAAAATGATATGGATACTCGCTATACTTCCTATCCT 2289

Qy        672 ProProThrLeuSerThrAspHisThrSerTrpGlyGlyTyrValTrpAlaGlyGluLeu 691

Db       2290 GAAGCT--------------CAAGGCTCTTGGACCAATAACTCTGGGGCTCTAGAGCTC 2334

Qy        692 GlyThrArgValAlaValGluAsnThrSerGlyArgGlyPhePheGlnGluTyrThrPro 711

Db       2335 GGAGGATCTCTGGCTCTATATCTCCCTAAAGAAGCACCGTTCTTCCAGGGATATTTCCCC 2394

Qy        712 PheValLysValGlnAlaValTyrAlaArgGlnAspSerPheValGluLeuGlyAlaIle 731

Db       2395 TTCTTAAAGTTCCAGGCAGTCTACAGCCGCCAACAAAACTTTAAAGAGAGTGGCGCTGAA 2454

Qy        732 SerArgAspPheSerAspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLysLeu 751

Db       2455 GCCCGTGCTTTTGATGATGGAGACCTAGTGAACTGCTCTATCCCTGTCGGCATTCGGTTA 2514

Qy        752 GluLysArgPheAlaGluGln------TyrTyrHisValValAlaMetTyrSerProAsp 769

Db       2515 GAAAAAATCTCCGAAGATGAAAAAAATAATTTCGAGATTTCTCTAGCCTACATTGGTGAT 2574

Qy        770 ValCysArgSerAsnProLysCysThrThrThrLeuLeuSerAsnGlnGlySerTrpLys 789

Db       2575 GTGTATCGTAAAAATCCCCGTTCGCGTACTTCTCTAATGGTCAGTGGAGCCTCTTGGACT 2634

Qy        790 ThrLysGlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSer 809

Db       2635 TCGCTATGTAAAAACCTCGCACGACAAGCCTTCTTAGCAAGTGCTGGAAGCCATCTGACT 2694

Qy        810 LeuGlyAlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArg 829

Db       2695 CTCTCCCCTCATGTAGAACTCTCTGGGGAAGCTGCTTATGAGCTTCGTGGCTCAGCACAC 2754

Qy        830 SerTyrAsnValAspAlaGlySerLysIleLysPhe 841

Db       2755 ATCTACAATGTAGATTGTGGGCTAAGATACTCATTC 2790
```

RESULT 8
US-10-312-273-96
; Sequence 96, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035WO
; CURRENT APPLICATION NUMBER: US/10/312,273
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 96
; LENGTH: 2787
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-96

Alignment Scores:

Pred. No.:	5.82e-134	Length:	2787
Score:	1407.50	Matches:	330
Percent Similarity:	51.04%	Conservative:	162
Best Local Similarity:	34.23%	Mismatches:	313
Query Match:	32.77%	Indels:	159
DB:	12	Gaps:	23

US-09-830-446-27 (1-841) x US-10-312-273-96 (1-2787)

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Qy          1 MetLysIleProLeuArgPheLeuLeuIle---SerLeuValProThrLeuSerMetSer 19

Db          1 ATGAAATCGCAATTTTCCTGGTTAGTGCTCTCTTCGACATTGGCATGTTTTACTAGTTGT 60

Qy         20 AsnLeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThr 39

Db         61 TCCACTGTTTTTGCTGCAACTGCTGAAAATATAGGCCCCTCTGATAGCTTTGACGGAAGT 120

Qy         40 ThrSerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrVal 59

Db        121 ACTAACACAGGCACCTATACTCCTAAA------AATACGACTACTGGAATAGACTATACT 174
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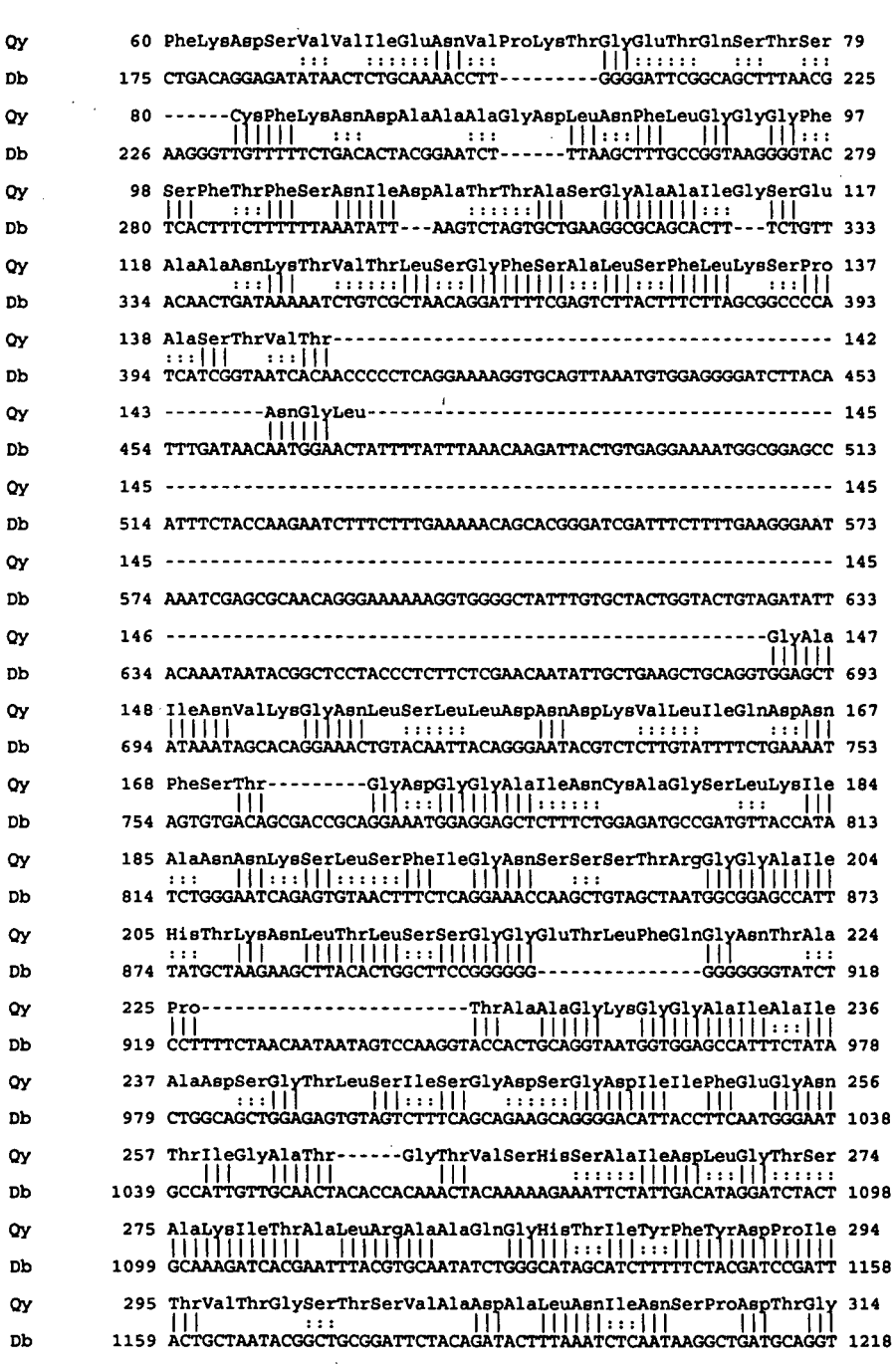
Qy 60 PheLysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSer 79
Db 175 CTGACAGGAGATATAACTCTGCAAAACCTT---------GGGGATTCGGCAGCTTTAACG 225
Qy 80 ------CysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPhe 97
Db 226 AAGGGTTGTTTTTCTGACACTACGGAATCT------TTAAGCTTTGCCGGTAAGGGGTAC 279
Qy 98 SerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGlu 117
Db 280 TCACTTTCTTTTTTAAATATT---AAGTCTAGTGCTGAAGGCGCAGCACTT---TCTGTT 333
Qy 118 AlaAlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerPro 137
Db 334 ACAACTGATAAAAATCTGTCGCTAACAGGATTTTCGAGTCTTACTTTCTTAGCGGCCCCA 393
Qy 138 AlaSerThrValThr---------- 142
Db 394 TCATCGGTAATCACAACCCCCTCAGGAAAAGGTGCAGTTAAATGTGGAGGGGATCTTACA 453
Qy 143 ---------AsnGlyLeu---------- 145
Db 454 TTTGATAACAATGGAACTATTTTATTTAAACAAGATTACTGTGAGGAAAATGGCGGAGCC 513
Qy 145 ---------- 145
Db 514 ATTTCTACCAAGAATCTTTCTTTGAAAAACAGCACGGGATCGATTTCTTTTGAAGGGAAT 573
Qy 145 ---------- 145
Db 574 AAATCGAGCGCAACAGGGAAAAAAGGTGGGGCTATTTGTGCTACTGGTACTGTAGATATT 633
Qy 146 ----------GlyAla 147
Db 634 ACAAATAATACGGCTCCTACCCTCTTCTCGAACAATATTGCTGAAGCTGCAGGTGGAGCT 693
Qy 148 IleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsn 167
Db 694 ATAAATAGCACAGGAAACTGTACAATTACAGGGAATACGTCTCTTGTATTTTCTGAAAAT 753
Qy 168 PheSerThr---------GlyAspGlyGlyAlaIleAsnCysAlaGlySerLeuLysIle 184
Db 754 AGTGTGACAGCGACCGCAGGAAATGGAGGAGCTCTTTCTGGAGATGCCGATGTTACCATA 813
Qy 185 AlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArgGlyGlyAlaIle 204
Db 814 TCTGGGAATCAGAGTGTAACTTTCTCAGGAAACCAAGCTGTAGCTAATGGCGGAGCCATT 873
Qy 205 HisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAla 224
Db 874 TATGCTAAGAAGCTTACACTGGCTTCCGGGGGG----------GGGGGGGTATCT 918
Qy 225 Pro----------ThrAlaAlaGlyLysGlyGlyAlaIleAlaIle 236
Db 919 CCTTTTCTAACAATAATAGTCCAAGGTACCACTGCAGGTAATGGTGGAGCCATTTCTATA 978
Qy 237 AlaAspSerGlyThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsn 256
Db 979 CTGGCAGCTGGAGAGTGTAGTCTTTCAGCAGAAGCAGGGGACATTACCTTCAATGGGAAT 1038
Qy 257 ThrIleGlyAlaThr------GlyThrValSerHisSerAlaIleAspLeuGlyThrSer 274
Db 1039 GCCATTGTTGCAACTACACCACAAACTACAAAAAGAAATTCTATTGACATAGGATCTACT 1098
Qy 275 AlaLysIleThrAlaLeuArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIle 294
Db 1099 GCAAAGATCACGAATTTACGTGCAATATCTGGGCATAGCATCTTTTTCTACGATCCGATT 1158
Qy 295 ThrValThrGlySerThrSerValAlaAspAlaLeuAsnIleAsnSerProAspThrGly 314
Db 1159 ACTGCTAATACGGCTGCGGATTCTACAGATACTTTAAATCTCAATAAGGCTGATGCAGGT 1218
Qy 315 AspAsnLysGluTyrThrGlyThrIleValPheSerGlyGluLysLeuThrGluAlaGlu 334
Db 1219 AATAGTACAGATTATAGTGGGTCGATTGTTTTTTCTGGTGAAAAGCTCTCTGAAGATGAA 1278
Qy 335 AlaLysAspGluLysAsnArgThrSerLysLeuLeuGlnAsnValAlaPheLysAsnGly 354
Db 1279 GCAAAAGTTGCAGACAACCTCACTTCTACGCTGAAGCAGCCTGTAACTCTAACTGCAGGA 1338
Qy 355 ThrValValLeuLysGlyAspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsn 374
Db 1339 AATTTAGTACTTAAACGTGGTGTCACTCTCGATACGAAAGGCTTTACTCAGACCGCGGGT 1398
Qy 375 SerLysLeuIleMetAspLeuGlyThrSerLeuValAlaAsnThrGluSerIleGluLeu 394
Db 1399 TCCTCTGTTATTATGGATGCGGGCACAACGTTAAAAGCAAGTACAGAGGAGGTCACTTTA 1458
Qy 395 ThrAsnLeuGluIleAsnIleAspSerLeuArgAsnGlyLysLysIleLysLeuSerAla 414
Db 1459 ACAGGTCTTTCCATTCCTGTAGACTCTTTAGGCGAGGGTAAGAAAGTTGTAATTGCTGCT 1518
Qy 415 AlaThrAlaGlnLysAspIleArgIleAspArgProValValLeuAlaIleSerAspGlu 434
Db 1519 TCTGCAGCAAGTAAAAATGTAGCCCTTAGTGGTCCGATTCTTCTTTTGGATAACCAAGGG 1578
Qy 435 SerPheTyrGlnAsnGlyPheLeuAsnGluAspHisSerTyrAspGlyIleLeuGluLeu 454
Db 1579 AATGCTTATGAAAATCACGACTTAGGAAAAACTCAAGACTTT---TCATTTGTGCAGCTC 1635
Qy 455 AspAlaGlyLysAspIleValIleSerAlaAspSerArgSerIleAspAlaValGlnSer 474
Db 1636 TCTGCT---CTGGGTACTGCAACAACTACAGATGTTCCAGCGGTTCCTACAGTAGCAACT 1692
Qy 475 Pro------TyrGlyTyrGlnGlyLysTrpThrIleAsnTrpSerThrAsp--------- 489
Db 1693 CCTACGCACTATGGGTATCAAGGTACTTGGGGAATGACTTGGGTTGATGATACCGCAAGC 1752
Qy 490 ---------AspLysLysAlaThrValSerTrpAlaLysGlnSerPheAsnProThrAla 506
Db 1753 ACTCCAAAGACTAAGACAGCGACATTAGCTTGGACCAATACAGGCTACCTTCCGAATCCT 1812
Qy 507 GluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySerPheIleAspValArgSer 526
Db 1813 GAGCGTCAAGGACCTTTAGTTCCTAATAGCCTTTGGGGATCTTTTTCAGACATCCAAGCG 1872
Qy 527 PheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTyrGluLysArgPheTrpVal 546
Db 1873 ATTCAAGGTGTCATAGAGAGAAGTGCTTTGACTCTTTGTTCAGATCGAGGCTTCTGGGCT 1932
Qy 547 AlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAsnGlnArgLysPheArgHis 566
Db 1933 GCGGGAGTCGCCAATTTCTTAGATAAAGATAAGAAAGGGGAAAAACGCAAATACCGTCAT 1992
Qy 567 ValSerGlyGlyAlaValValGlyAlaSerThrArgMetProGlyGlyAspThrLeuSer 586
Db 1993 AAATCTGGTGGATATGCTATCGGAGGTGCAGCGCAAACTTGTTCTGAAAACTTAATTAGC 2052
Qy 587 LeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPheMetAsnThrAsnPheAla 606
Db 2053 TTTGCCTTTTGCCAACTCTTTGGTAGCGATAAAGATTTCTTAGTCGCTAAAAATCATACT 2112
Qy 607 LysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSerLeuTyrSerValValSer 626
Db 2113 GATACCTATGCAGGAGCCTTCTATATCCAACACATTACAGAATGTAGTGGGTTCATAGGT 2172
Qy 627 IleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuProTyrValSerLysThrLeu 646
Db 2173 TGTCTCTTAGATAAA----------CTTCCTGGCTCTTGGAGTCATAAA 2211
Qy 647 ProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAspHisArgMetLysThrGlu 666
Db 2212 CCCCTCGTTTTAGAAGGGCAGCTCGCTTATAGCCACGTCAGTAATGATCTGAAGACAAAG 2271
Qy 667 SerLeuProProProProProThrLeuSerThrAspHisThrSerTrpGlyGlyTyrVal 686

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Db       2272 TATACTGCGTATCCTGAGGTG--------------AAAGGTTCTTGGGGGAATAATGCT 2316

Qy        687 TrpAlaGlyGluLeuGlyThrArgValAlaValGluAsnThrSerGlyArgGlyPhe--- 705

Db       2317 TTTAACATGATGTTGGGA--------------------GCTTCTTCTCATTCTTATCCT 2355

Qy        706 --------------PheGlnGluTyrThrProPheValLysValGlnAlaValTyrAla 720

Db       2356 GAATACCTGCATTGTTTTGATACCTATGCTCCATACATCAAACTGAATCTGACCTATATA 2415

Qy        721 ArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSerAspSerHisLeu 740

Db       2416 CGTCAGGACAGCTTCTCGGAGAAAGGTACAGAAGGAAGATCTTTTGATGACAGCAACCTC 2475

Qy        741 TyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPheAla---------Glu 757

Db       2476 TTCAATTTATCTTTGCCTATAGGGGTGAAGTTTGAGAAG---TTCTCTGATTGTAATGAC 2532

Qy        758 GlnTyrTyrHisValValAlaMetTyrSerProAspValCysArgSerAsnProLysCys 777

Db       2533 TTTTCTTATGATCTGACTTTATCCTATGTTCCTGATCTTATCCGCAATGATCCCAAATGC 2592

Qy        778 ThrThrThrLeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsnLeuAlaArg 797

Db       2593 ACTACAGCACTTGTAATCAGCGGAGCCTCTTGGGAAACTTATGCCAATAACTTAGCACGA 2652

Qy        798 GlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAlaGluLeuPhe 817

Db       2653 CAGGCCTTGCAAGTGCGTGCAGGCAGTCACTACGCCTTCTCTCCTATGTTTGAAGTGCTC 2712

Qy        818 GlyAsnPheGlyPheGluTrpArgGlySerSerArgSerTyrAsnValAspAlaGlySer 837

Db       2713 GGCCAGTTTGTCTTTGAAGTTCGTGGATCCTCACGGATTTATAATGTAGATCTTGGGGGT 2772

Qy        838 LysIleLysPhe 841

Db       2773 AAGTTCCAATTC 2784
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RESULT 9
US-10-312-273-34
; Sequence 34, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
;  FILE REFERENCE: P025035WO
;  CURRENT APPLICATION NUMBER: US/10/312,273
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: 0016363.4
;  PRIOR FILING DATE: 2000-07-03
;  PRIOR APPLICATION NUMBER: 0017047.2
;  PRIOR FILING DATE: 2000-07-11
;  PRIOR APPLICATION NUMBER: 0017983.8
;  PRIOR FILING DATE: 2000-07-21
;  PRIOR APPLICATION NUMBER: 0019368.0
;  PRIOR FILING DATE: 2000-08-07
;  PRIOR APPLICATION NUMBER: 0020440.4
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;  PRIOR APPLICATION NUMBER: 0027549.5
;  PRIOR FILING DATE: 2000-11-10
;  PRIOR APPLICATION NUMBER: 0031706.5
;  PRIOR FILING DATE: 2000-12-22
;  NUMBER OF SEQ ID NOS: 664
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 34
;   LENGTH: 2787
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-312-273-34
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Alignment Scores:
Pred. No.:                4.39e-131      Length:          2787
Score:                    1379.50        Matches:         348
Percent Similarity:       49.53%         Conservative:    124
Best Local Similarity:    36.52%         Mismatches:      344
Query Match:              32.12%         Indels:          137
DB:                       12             Gaps:            22

US-09-830-446-27 (1-841) x US-10-312-273-34 (1-2787)

Qy          1 MetLysIleProLeuArgPheLeuLeuIle------SerLeuValProThrLeuSerMet 18

Db          1 ATGAAATCCTCTCTTCATTGGTTTTTAATCTCGTCATCTTTAGCACTTCCCTTGTCACTA 60

Qy         19 SerAsnLeuLeuGlyAlaAlaThrThrGlu---GluLeuSerAlaSerAsnSerPheAsp 37

Db         61 AATTTCTCTGCGTTTGCTGCTGTTGTTGAAATCAATCTAGGACCTACCAATAGCTTCTCT 120

Qy         38 GlyThrThrSerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsn 57

Db        121 GGACCAGGAACCTACACTCCTCCAGCCCAAACAACAAATGCA------GATGGAACTATC 174

Qy         58 TyrValPheLysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSer 77

Db        175 TATAATCTAACAGGGGATGTCTCAATCACCAATGCA---GGATCTCCGACAGCTCTAACC 231

Qy         78 ThrSerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPhe 97

Db        232 GCTTCCTGCTTTAAAGAA------ACTACTGGGAATCTTTCTTTCCAAGGCCACGGCTAC 285

Qy         98 SerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGlu 117

Db        286 CAATTTCTCCTACAAAATATCGATGCG------GGAGCGAACTGTACCTTTACCAATACA 339

Qy        118 AlaAlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerPro 137

Db        340 GCTGCAAATAAGCTTCTCTCCTTTTCAGGATTCTCCTATTTGTCACTAATACAAACC--- 396

Qy        138 AlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeu 157

Db        397 ---ACGAATGCTACCACAGGAACAGGAGCCATCAAGTCCACAGGAGCTTGTTCTATTCAG 453

Qy        158 AspAsnAspLysValLeuIleGlnAspAsnPheSer---------------------- 169

Db        454 TCGAACTATAGTTGCTACTTTGGCCAAAACTTTTCTAATGACAATGGAGGCGCCCTCCAA 513

Qy        169 ---------------------------------------------------------- 169

Db        514 GGCAGCTCTATCAGTCTATCGCTAAACCCCAACCTAACGTTTGCCAAAAACAAAGCAACG 573

Qy        169 ---------------------------------------------------------- 169

Db        574 CAAAAAGGGGGTGCCCTCTATTCCACGGGAGGGATTACAATTAACAATACGTTAAACTCA 633

Qy        169 ---------------------------------------------------------- 169

Db        634 GCATCATTTTCTGAAAATACCGCGGCGAACAATGGCGGAGCCATTTACACGGAAGCTAGC 693

Qy        170 ----------------------------------------------------------Thr 170

Db        694 AGTTTTATTAGCAGCAACAAAGCAATTAGCTTTATAAACAATAGTGTGACCGCAACCTCA 753

Qy        171 GlyAspGlyGlyAlaIleAsnCysAlaGlySer------------------LeuLysIle 184

Db        754 GCTACAGGGGGAGCCATTTACTGTAGTAGTACATCAGCCCCCAAACCAGTCTTAACTCTA 813

Qy        185 AlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArgGlyGlyAlaIle 204

Db        814 TCAGACAACGGGGAACTGAACTTTATAGGAAATACAGCAATTACTAGTGGTGGGGCGATT 873

Qy        205 HisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAla 224

Db        874 TATACTGACAATCTAGTTCTTTCTTCTGGAGGACCTACGCTTTTTAAAAACAACTCTGCT 933
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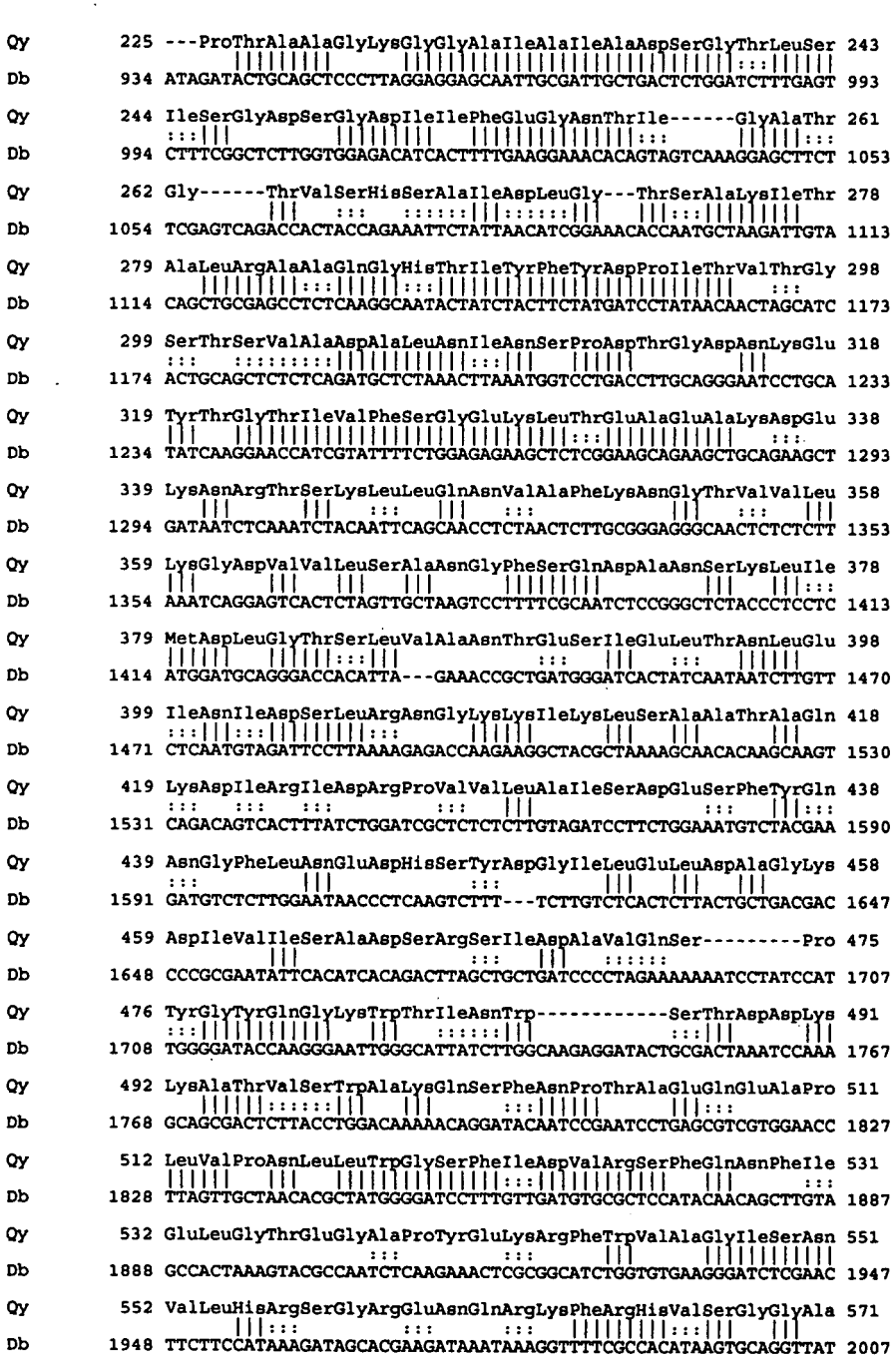

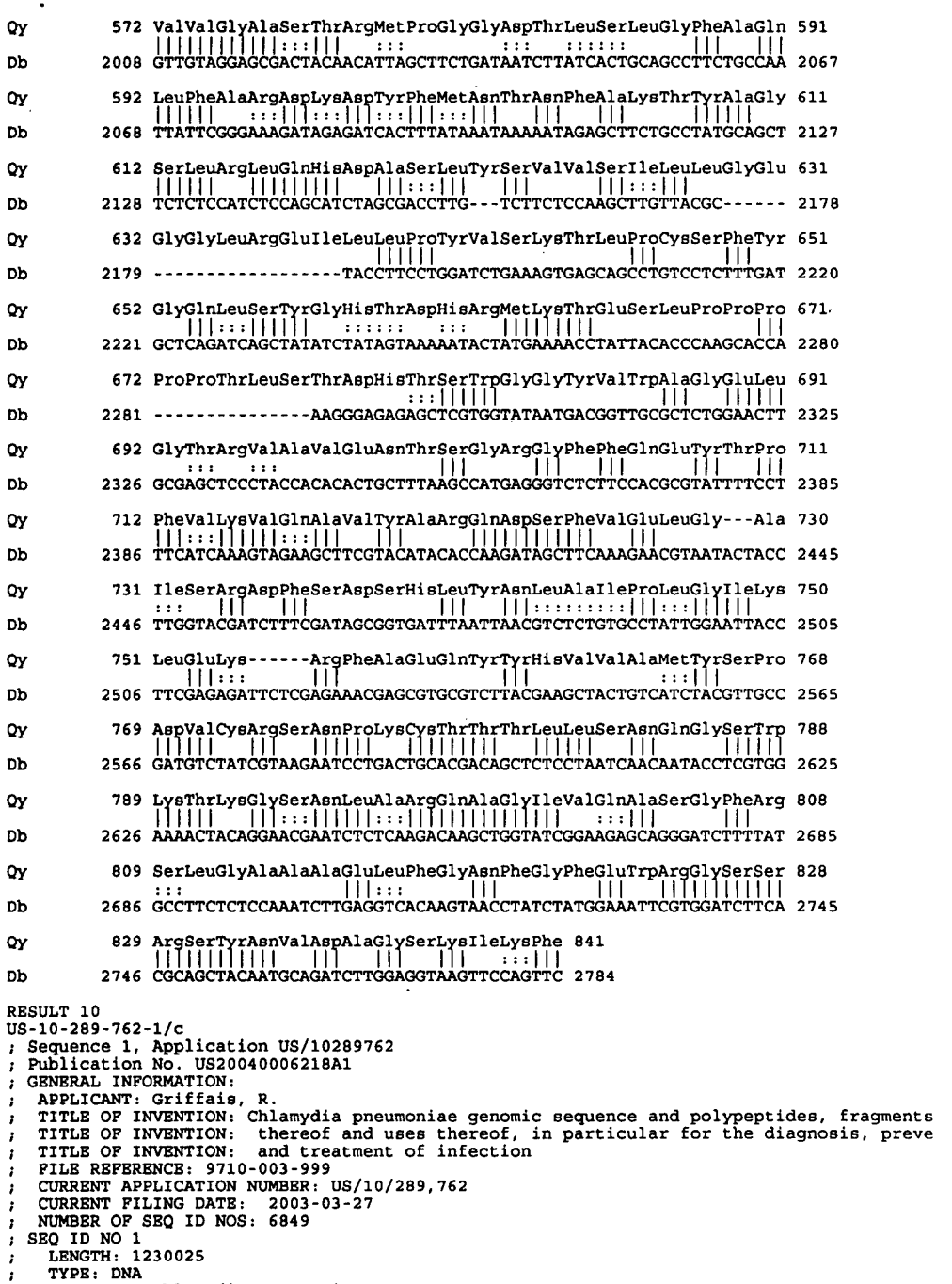

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; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae

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Alignment Scores:

Pred. No.:	1.72e-125	Length:	1230025
Score:	1365.00	Matches:	329
Percent Similarity:	51.04%	Conservative:	161
Best Local Similarity:	34.27%	Mismatches:	320
Query Match:	31.78%	Indels:	151
DB:	12	Gaps:	22

US-09-830-446-27 (1-841) x US-10-289-762-1 (1-1230025)

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Qy          1 MetLysIleProLeuArgPheLeuLeuIle---SerLeuValProThrLeuSerMetSer 19
              |||||              :::|||:::::   |||   :::         :::
Db     518200 ATGAAATCGCAATTTTCCTGGTTAGTGCTCTCTTCGACATTGGCATGTTTTACTAGTTGT 518141

Qy         20 AsnLeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThr 39
              :::   :::   |||||||||   |||   :::       |||:::|||||||||||::
Db     518140 TCCACTGTTTTTGCTGCAACTGCTGAAAATATAGGCCCCTCTGATAGCTTTGACGGAAGT 518081

Qy         40 ThrSerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrVal 59
              |||:::|||   :::::::::   |||       :::   |||   |||   :::|||
Db     518080 ACTAACACAGGCACCTATACTCCTAAA------AATACGACTACTGGAATAGACTATACT 518027

Qy         60 PheLysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSer 79
                         :::   :::::::|||:::       |||::::::   :::   :::
Db     518026 CTGACAGGAGATATAACTCTGCAAAACCTT---------GGGGATTCGGCAGCTTTAACG 517976

Qy         80 ------CysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPhe 97
                 ||||||   :::       :::       |||:::|||   |||   |||:::
Db     517975 AAGGGTTGTTTTTCTGACACTACGGAATCT------TTAAGCTTTGCCGGTAAGGGGTAC 517922

Qy         98 SerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGlu 117
              |||   :::|||   |||         :::::::|||   ||||||   :::   |||
Db     517921 TCACTTTCTTTTTTAAAT---ATNAAGTCTAGTGCTGAAGGCGCANA-CTT---TCTGTT 517869
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Qy        118 AlaAlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerPro 137
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Db     517868 ACAACTGATAAAAATCTGTCGCTAACAGGATTTTCGAGTCTTACTTTCTTAGCGGCCCCA 517809

Qy        138 AlaSerThrValThr---------------------------------------------- 142
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Db     517808 TCATCGGTAATCACAACCCCCTCAGGAAAAGGTGCAGTTAAATGTGGAGGGGATCTTACA 517749

Qy        143 ---------AsnGly-Leu------------------------------------------ 145
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Db     517748 TTTGATAACAATGGAACTATTTTATTTAAACAAGATTACTGTGAGGAAAATGGCGGACAT 517689

Qy        145 ------------------------------------------------------------ 145

Db     517688 TTCTACCAAGAATCTTTCTTTGAAAAACAGCACGGGATCGATTTCTTTTGAAGGGAATAA 517629

Qy        145 ------------------------------------------------------------ 145

Db     517628 ATCGAGCGCAACAGGGAAAAAAGGTGGGGCTATTTGTGCTACTGGTACTGTAGATATTAC 517569

Qy        146 ----------------------------------------------------GlyAlaIl 148
                                                                   ||||||||
Db     517568 AAATAATACGGCTCCTACCCTCTTCTCGAACAATATTGCTGAAGCTGCAGGTGGAGCTAT 517509

Qy        148 eAsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsnPh 168
              ||||      ||||||  ::::::      |||      ::::::      :::|||
Db     517508 AAATAGCACAGGAAACTGTACAATTACAGGGAATACGTCTCTTGTATTTTCTGAAAATAG 517449

Qy        168 eSerThr---------GlyAspGlyGlyAlaIleAsnCysAlaGlySerLeuLysIleAl 185
                 |||          |||::|||||||||::::::           :::   |||::
Db     517448 TGTGACAGCGACCGCAGGAAATGGAGGAGCTCTTTCTGGAGATGCCGATGTTACCATATC 517389

Qy        185 aAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArgGlyGlyAlaIleHi 205
              :  |||:::|||::::::|||  ||||||  :::          ||||||||||||::
Db     517388 TGGGAATCAGAGTGTAACTTTCTCAGGAAACCAAGCTGTAGCTAATGGCGGAGCCATTTA 517329

Qy        205 sThrLysAsnLeuThrLeuSerSer---------GlyGlyGluThrLeuPhe-GlnGlyA 222
              :  |||   |||||||||:::|||         ||||||      ||||||
Db     517328 TGCTAAGAAGCTTACACTGGCTTCCGGGGGGGGGGGGGGGTATCTCCTTTTCTAACAATA 517269

Qy        222 snThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGlyThrL 242
                       |||   ||||||   ||||||||||||:::|||      :::|||
Db     517268 TAGTCCAAGGTACCACTGCAGGTAATGGTGGAGCCATTTCTATACTGGCAGCTGGAGAGT 517209

Qy        242 euSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAlaThr- 261
              |||:::|||   ::::::||||||||   |||   ||||||   |||   ||||||
Db     517208 GTAGTCTTTCAGCAGAAGCAGGGGACATTACCTTCAATGGGAATGCCATTGTTGCAACTA 517149

Qy        262 -----GlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaL 280
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Qy        280 euArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGlySerT 300
              ||||||||      ||||||:::|||:::|||||||||||||||||||         :::
Db     517088 TACGTGCAATATCTGGGCATAGCATCTTTTTCTACGATCCGATTACTGCTAATACGGCTG 517029

Qy        300 hrSerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGluTyrT 320
                    |||   ||||||:::|||       |||   |||::::::   :::|||:
Db     517028 CGGATTCTACAGATACTTTAAATCTCAATAAGGCTGATGCAGGTAATAGTACAGATTATA 516969

Qy        320 hrGlyThrIleValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGluLysA 340
              ::|||:::|||||||||||||||||||||||:::|||   |||||||||         |
Db     516968 GTGGGTCGATTGTTTTTTCTGGTGAAAAGCTCTCTGAAGATGAAGCAAAAGTTGCAGACA 516909

Qy        340 snArgThrSerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLysG 360
              ||   ||||||   |||   |||   |||              |||   :::||||||||
Db     516908 ACCTCACTTCTACGCTGAAGCAGCCTGTAACTCTAACTGCAGGAAATTTAGTACTTAAAC 516849

Qy        360 lyAspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetA 380
                 |||   |||         |||||||:::|||   |||   |||   :::||||||||
Db     516848 GTGGTGTCACTCTCGATACGAAAGGCTTTACTCAGACCGCGGGTTCCTCTGTTATTATGG 516789
```

```
Qy      380 spLeuGlyThrSerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleA 400
Db   516788 ATGCGGGCACAACGTTAAAAGCAAGTACAGAGGAGGTCACTTTAACAGGTCTTTCCATTC 516729

Qy      400 snIleAspSerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysA 420
Db   516728 CTGTAGACTCTTTAGGCGAGGGTAAGAAAGTTGTAATTGCTGCTTCTGCAGCAAGTAAAA 516669

Qy      420 spIleArgIleAspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsnG 440
Db   516668 ATGTAGCCCTTAGTGGTCCGATTCTTCTTTTGGATAACCAAGGGAATGCTTATGAAAATC 516609

Qy      440 lyPheLeuAsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspI 460
Db   516608 ACGACTTAGGAAAAACTCAAGACTTT---TCATTTGTGCAGCTCTCTGCT---CTGGGTA 516555

Qy      460 leValIleSerAlaAspSerArgSerIleAspAlaValGlnSerPro------TyrGlyT 478
Db   516554 CTGCAACAACTACAGATGTTCCAGCGGTTCCTACAGTAGCAACTCCTACGCACTATGGGT 516495

Qy      478 yrGlnGlyLysTrpThrIleAsnTrpSerThrAsp----------------AspLysL 492
Db   516494 ATCAAGGTACTTGGGGAATGACTTGGGTTGATGATACCGCAAGCACTCCAAAGACTAAGA 516435

Qy      492 ysAlaThrValSerTrpAlaLysGlnSerPheAsnProThrAlaGluGlnGluAlaProL 512
Db   516434 CAGCGACATTAGCTTGGACCAATACGGGCTACCTTCCGAATCCTGAGCGTCAAGGACCTT 516375

Qy      512 euValProAsnLeuLeuTrpGlySerPheIleAspValArgSerPheGlnAsnPheIleG 532
Db   516374 TAGTTCCTAATAGCCTTTGGGGATCTTTTTCAGACATCCAAGCGATTCAAGGTGTCATAG 516315

Qy      532 luLeuGlyThrGluGlyAlaProTyrGluLysArgPheTrpValAlaGlyIleSerAsnV 552
Db   516314 AGAGAAGTGCTTTGACTCTTTGTTCAGATCGAGGCTTCTGGGCTGCGGGAGTCGCCAATT 516255

Qy      552 alLeuHisArgSerGlyArgGluAsnGlnArgLysPheArgHisValSerGlyGlyAlaV 572
Db   516254 TCTTAGATAAAGATAAGAAAGGGGAAAAACGCAAATACCGTCATAAATCTGGTGGATATG 516195

Qy      572 alValGlyAlaSerThrArgMetProGlyGlyAspThrLeuSerLeuGlyPheAlaGlnL 592
Db   516194 CTATCGGAGGTGCAGCGCAAACTTGTTCTGAAAACTTAATTAGCTTTGCCTTTTGCCAAC 516135

Qy      592 euPheAlaArgAspLysAspTyrPheMetAsnThrAsnPheAlaLysThrTyrAlaGlyS 612
Db   516134 TCTTTGGTAGCGATAAAGATTTCTTAGTCGCTAAAAATCATACTGATACCTATGCAGGAG 516075

Qy      612 erLeuArgLeuGlnHisAspAlaSerLeuTyrSerValValSerIleLeuLeuGlyGluG 632
Db   516074 CCTTCTATATCCAACACATTACAGAATGTAGTGGGTTCATAGGTTGTCTCTTAGATAAA- 516016

Qy      632 lyGlyLeuArgGluIleLeuLeuProTyrValSerLysThrLeuProCysSerPheTyrG 652
Db   516015 ------------------CTTCCTGGCTCTTGGAGTCATAAACCCCTCGTTTTAGAAG 515976

Qy      652 lyGlnLeuSerTyrGlyHisThrAspHisArgMetLysThrGluSerLeuProProProP 672
Db   515975 GGCAGCTCGCTTATAGCCACGTCAGTAATGATCTGAAGACAAAGTATACTGCGTATCCTG 515916

Qy      672 roProThrLeuSerThrAspHisThrSerTrpGlyGlyTyrValTrpAlaGlyGluLeuG 692
Db   515915 AGGTG--------------AAAGGTTCTTGGGGGAATAATGCTTTTAACATGATGTTGG 515871

Qy      692 lyThrArgValAlaValGluAsnThrSerGlyArgGlyPhe----------------P 706
Db   515870 GA------------------GCTTCTTCTCATTCTTATCCTGAATACCTGCATTGTT 515832

Qy      706 heGlnGluTyrThrProPheValLysValGlnAlaValTyrAlaArgGlnAspSerPheV 726
Db   515831 TTGATACCTATGCTCCATACATCAAACTGAATCTGACCTATATACGTCAGGACAGCTTCT 515772

Qy      726 alGluLeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyrAsnLeuAlaIleP 746
Db   515771 CGGAGAAAGGTACAGAAGGAAGATCTTTTGATGACAGCAACCTCTTCAATTTATCTTTGC 515712

Qy      746 roLeuGlyIleLysLeuGluLysArgPheAla---------GluGlnTyrTyrHisValV 763
Db   515711 CTATAGGGGTGAAGTTTGAGAAG---TTCTCTGATTGTAATGACTTTTCTTATGATCTGA 515655

Qy      763 alAlaMetTyrSerProAspValCysArgSerAsnProLysCysThrThrThrLeuLeuS 783
Db   515654 CTTTATCCTATGTTCCTGATCTTATCCGCAATGATCCCAAATGCACTACAGCACTTGTAA 515595

Qy      783 erAsnGlnGlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAlaGlyIleValG 803
Db   515594 TCAGCGGAGCCTCTTGGGAAACTTATGCCAATAACTTAGCACGACAGGCCTTGCAAGTGC 515535

Qy      803 lnAlaSerGlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsnPheGlyPheG 823
Db   515534 GTGCAGGCAGTCACTACGCCTTCTCTCCTATGTTTGAAGTGCTCGGCCAGTTTGTCTTTG 515475

Qy      823 luTrpArgGlySerSerArgSerTyrAsnValAspAlaGlySerLysIleLysPhe 841
Db   515474 AAGTTCGTGGATCCTCACGGATTTATAATGTAGATCTTGGGGGTAAGTTCCAATTC 515419
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RESULT 11
US-10-312-273-20
; Sequence 20, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035WO
; CURRENT APPLICATION NUMBER: US/10/312,273
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 20
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-20

Alignment Scores:

Pred. No.:	5.71e-129	Length:	2241
Score:	1357.50	Matches:	330
Percent Similarity:	56.17%	Conservative:	116
Best Local Similarity:	41.56%	Mismatches:	270
Query Match:	31.61%	Indels:	78
DB:	12	Gaps:	21

US-09-830-446-27 (1-841) x US-10-312-273-20 (1-2241)

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Qy       75 ThrGlnSerThrSerCysPheLysAsnAspAla------AlaAlaGlyAspLeuAsnPhe 92
Db       16 TCTGAAAATACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTACCATT 75

Qy       93 LeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAla 112
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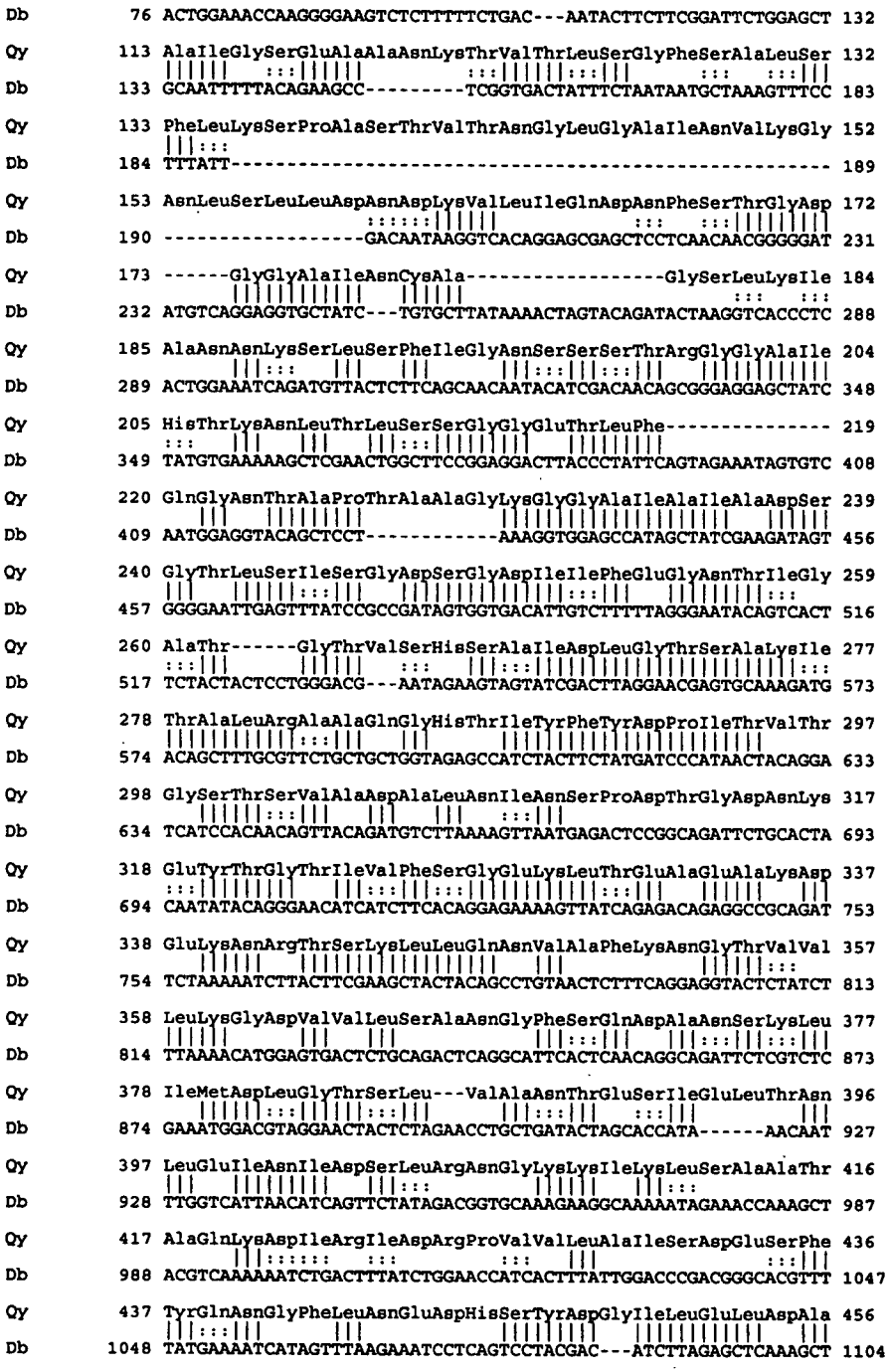
Db 76 ACTGGAAACCAAGGGGAAGTCTCTTTTTCTGAC---AATACTTCTTCGGATTCTGGAGCT 132
Qy 113 AlaIleGlySerGluAlaAlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSer 132
Db 133 GCAATTTTTACAGAAGCC---------TCGGTGACTATTTCTAATAATGCTAAAGTTTCC 183
Qy 133 PheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValLysGly 152
Db 184 TTTATT---------- 189
Qy 153 AsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsnPheSerThrGlyAsp 172
Db 190 ----------GACAATAAGGTCACAGGAGCGAGCTCCTCAACAACGGGGGAT 231
Qy 173 ------GlyGlyAlaIleAsnCysAla----------GlySerLeuLysIle 184
Db 232 ATGTCAGGAGGTGCTATC---TGTGCTTATAAAACTAGTACAGATACTAAGGTCACCCTC 288
Qy 185 AlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArgGlyGlyAlaIle 204
Db 289 ACTGGAAATCAGATGTTACTCTTCAGCAACAATACATCGACAACAGCGGGAGGAGCTATC 348
Qy 205 HisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPhe---------- 219
Db 349 TATGTGAAAAAGCTCGAACTGGCTTCCGGAGGACTTACCCTATTCAGTAGAAATAGTGTC 408
Qy 220 GlnGlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSer 239
Db 409 AATGGAGGTACAGCTCCT-----------AAAGGTGGAGCCATAGCTATCGAAGATAGT 456
Qy 240 GlyThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGly 259
Db 457 GGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGTCTTTTTAGGGAATACAGTCACT 516
Qy 260 AlaThr------GlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIle 277
Db 517 TCTACTACTCCTGGGACG---AATAGAAGTAGTATCGACTTAGGAACGAGTGCAAAGATG 573
Qy 278 ThrAlaLeuArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThr 297
Db 574 ACAGCTTTGCGTTCTGCTGCTGGTAGAGCCATCTACTTCTATGATCCCATAACTACAGGA 633
Qy 298 GlySerThrSerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLys 317
Db 634 TCATCCACAACAGTTACAGATGTCTTAAAAGTTAATGAGACTCCGGCAGATTCTGCACTA 693
Qy 318 GluTyrThrGlyThrIleValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAsp 337
Db 694 CAATATACAGGGAACATCATCTTCACAGGAGAAAAGTTATCAGAGACAGAGGCCGCAGAT 753
Qy 338 GluLysAsnArgThrSerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValVal 357
Db 754 TCTAAAAATCTTACTTCGAAGCTACTACAGCCTGTAACTCTTTCAGGAGGTACTCTATCT 813
Qy 358 LeuLysGlyAspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeu 377
Db 814 TTAAAACATGGAGTGACTCTGCAGACTCAGGCATTCACTCAACAGGCAGATTCTCGTCTC 873
Qy 378 IleMetAspLeuGlyThrSerLeu---ValAlaAsnThrGluSerIleGluLeuThrAsn 396
Db 874 GAAATGGACGTAGGAACTACTCTAGAACCTGCTGATACTAGCACCATA------AACAAT 927
Qy 397 LeuGluIleAsnIleAspSerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThr 416
Db 928 TTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGAAGGCAAAAATAGAAACCAAAGCT 987
Qy 417 AlaGlnLysAspIleArgIleAspArgProValValLeuAlaIleSerAspGluSerPhe 436
Db 988 ACGTCAAAAAATCTGACTTTATCTGGAACCATCACTTTATTGGACCCGACGGGCACGTTT 1047
Qy 437 TyrGlnAsnGlyPheLeuAsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAla 456
Db 1048 TATGAAAATCATAGTTTAAGAAATCCTCAGTCCTACGAC---ATCTTAGAGCTCAAAGCT 1104
Qy 457 GlyLysAspIleValIleSerAla--AspSerArgSerIleAspAlaValGlnSerPro- 475
Db 1105 TCTGGAACTGTAACAAGCACCGCAGTGACTCCAGATCCTATAATGGGTGAGAAATTCCAT 1164
Qy 476 TyrGlyTyrGlnGlyLysTrp---ThrIleAsnTrpSerThrAsp---AspLysLysAla 493
Db 1165 TACGGCTATCAGGGAACTTGGGGCCCAATTGTTTGGGGGACAGGGGCTTCTACGACTGCA 1224
Qy 494 ThrValSerTrpAlaLysGlnSerPheAsnProThrAlaGluGlnGluAlaProLeuVal 513
Db 1225 ACCTTCAACTGGACTAAAACTGGCTATATTCCTAATCCCGAGCGTATCGGCTCTTTAGTC 1284
Qy 514 ProAsnLeuLeuTrpGlySerPheIleAspValArgSerPheGlnAsnPheIleGluLeu 533
Db 1285 CCTAATAGCTTATGGAATGCATTTATAGATATTAGCTCTCTCCATTATCTTATGGAGACT 1344
Qy 534 GlyThrGluGlyAlaProTyrGluLysArgPheTrpValAlaGlyIleSerAsnValLeu 553
Db 1345 GCAAACGAAGGGTTGCAGGGAGACCGTGCTTTTTGGTGTGCTGGATTATCTAACTTCTTC 1404
Qy 554 HisArgSerGlyArgGluAsnGlnArgLysPheArgHisValSerGlyGlyAlaValVal 573
Db 1405 CATAAGGATAGTACAAAAACACGACGCGGGTTTCGCCATTTGAGTGGCGGTTATGTCATA 1464
Qy 574 GlyAlaSerThrArgMetProGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPhe 593
Db 1465 GGAGGAAACCTACATACTTGTTCAGATAAGATTCTTAGTGCTGCATTTTGTCAGCTCTTT 1524
Qy 594 AlaArgAspLysAspTyrPheMetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeu 613
Db 1525 GGAAGAGATAGAGACTACTTTGTAGCTAAGAATCAAGGTACAGTCTACGGAGGAACTCTC 1584
Qy 614 ArgLeuGlnHisAspAlaSerLeuTyrSerValValSerIleLeuLeuGlyGluGlyGly 633
Db 1585 TATTACCAGCACAACGAAACCTATATCTCTCTTCCTTGC----------AAA 1626
Qy 634 LeuArgGluIleLeuLeuProTyrValSerLysThrLeuProCysSerPheTyrGlyGln 653
Db 1627 CTACGGCCTTGTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCTCTTTTCAGGAAAC 1686
Qy 654 LeuSerTyrGlyHisThrAspHisArgMetLysThrGluSerLeuProProProProPro 673
Db 1687 CTTAGCTACACCCATACGGATAACGATCTGAAAACCAAGTAT----------ACA 1731
Qy 674 ThrLeuSerThrAspHisThrSerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThr 693
Db 1732 ACATATCCTACTGTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTAGAATTCGGTGGA 1791
Qy 694 Arg------ValAlaValGluAsnThrSerGlyArgGlyPhePheGlnGluTyrThrPro 711
Db 1792 AGAGCTCCGATTTGCTTAGATGAAAGTGCT---------CTATTTGAGCAGTACATGCCC 1842
Qy 712 PheValLysValGlnAlaValTyrAlaArgGlnAspSerPheValGluLeuGlyAlaIle 731
Db 1843 TTCATGAAATTGCAGTTTGTCTATGCACATCAGGAAGGTTTTAAAGAACAGGGAACAGAA 1902
Qy 732 SerArgAspPheSerAspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLysLeu 751
Db 1903 GCTCGTGAATTTGGAAGTAGCCGTCTTGTGAATCTTGCCTTACCTATCGGGATCCGATTT 1962
Qy 752 GluLysArg------PheAlaGluGlnTyrTyrHisValValAlaMetTyrSerProAsp 769
Db 1963 GATAAGGAATCAGACTGCCAAGATGCAACGTACAATCTAACTCTTGGTTATACTGTGGAT 2022
Qy 770 ValCysArgSerAsnProLysCysThrThrThrLeuLeuSerAsnGlnGlySerTrpLys 789
Db 2023 CTTGTTCGTAGTAACCCCGACTGTACGACAACACTGCGAATTAGCGGTGATTCTTGGAAA 2082
Qy 790 ThrLysGlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSer 809
Db 2083 ACCTTCGGTACGAATTTGGCAAGACAAGCTTTAGTCCTTCGTGCAGGGAACCATTTTTGC 2142

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Qy        810 LeuGlyAlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArg 829
Db       2143 TTTAACTCAAATTTTGAAGCCTTTAGCCAATTTTCTTTTGAATTGCGTGGGTCATCTCGC 2202

Qy        830 SerTyrAsnValAspAlaGlySerLysIleLysPhe 841
Db       2203 AATTACAATGTAGACTTAGGAGCAAAATACCAATTC 2238

RESULT 12
US-10-312-273-154
; Sequence 154, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
;  FILE REFERENCE: P025035WO
;  CURRENT APPLICATION NUMBER: US/10/312,273
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: 0016363.4
;  PRIOR FILING DATE: 2000-07-03
;  PRIOR APPLICATION NUMBER: 0017047.2
;  PRIOR FILING DATE: 2000-07-11
;  PRIOR APPLICATION NUMBER: 0017983.8
;  PRIOR FILING DATE: 2000-07-21
;  PRIOR APPLICATION NUMBER: 0019368.0
;  PRIOR FILING DATE: 2000-08-07
;  PRIOR APPLICATION NUMBER: 0020440.4
;  PRIOR FILING DATE: 2000-08-18
;  PRIOR APPLICATION NUMBER: 0022583.9
;  PRIOR FILING DATE: 2000-09-14
;  PRIOR APPLICATION NUMBER: 0027549.5
;  PRIOR FILING DATE: 2000-11-10
;  PRIOR APPLICATION NUMBER: 0031706.5
;  PRIOR FILING DATE: 2000-12-22
;  NUMBER OF SEQ ID NOS: 664
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 154
;   LENGTH: 2811
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-312-273-154

Alignment Scores:
Pred. No.:                1.48e-126      Length:          2811
Score:                    1335.50        Matches:         311
Percent Similarity:       49.26%         Conservative:    157
Best Local Similarity:    32.74%         Mismatches:      359
Query Match:              31.09%         Indels:          123
DB:                       12             Gaps:            14

US-09-830-446-27 (1-841) x US-10-312-273-154 (1-2811)

Qy          1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
Db          1 ATGAAGTCCTCTGTCTCTTGGTTGTTCTTTTCTTCAATCCCGCTCTTTTCATCGCTCTCT 60

Qy         21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
Db         61 ATAGTCGCGGCAGAGGTGACCTTAGAT---AGCAGCAATAATAGCTATGATGGATCTAAC 117

Qy         41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
Db        118 GGAACTACCTTCACGGTCTTTTCCACTACGGACGCTGCTGCAGGAACTACCTATTCCTTA 177

Qy         61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCys 80
Db        178 CTTTCCGACGTATCCTTTCAAAATGCAGGGGCTTTAGGAATTCCCTTAGCCTCAGGATGC 237

Qy         81 PheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr 100
Db        238 TTCCTAGAA------GCGGGCGGCGATCTTACTTTCCAAGGAAATCAACATGCACTGAAG 291

Qy        101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsn 120
Db        292 TTTGCATTTATCAATGCGGGCTCTAGCGCTGGAACTGTAGCCAGTACCTCAGCAGCAGAT 351

Qy        121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
Db        352 AAGAATCTTCTCTTTAATGATTTTTCTAGACTCTCTATTATCTCTTGTCCCTCTCTTCTT 411

Qy        141 ValThr---AsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsn 159
Db        412 CTCTCTCCTACTGGACAATGTGCTTTAAAATCTGTGGGGAATCTATCTCTAACTGGCAAT 471

Qy        160 AspLysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsn------ 177
Db        472 TCCCAAATTATATTTACTCAGAACTTCTCGTCAGATAACGGCGGTGTTATCAATACGAAA 531

Qy        177 ------------------------------------------------------------ 177
Db        532 AACTTCTTATTATCAGGGACATCTCAGTTTGCGAGCTTTTCGAGAAACCAAGCCTTCACA 591

Qy        178 ----------------------CysAlaGlySerLeuLysIleAlaAsn--------- 186
Db        592 GGGAAGCAAGGCGGTGTAGTTTACGCTACAGGAACTATAACTATCGAGAACAGCCCTGGG 651

Qy        186 ------------------------------------------------------------ 186
Db        652 ATAGTTTCCTTCTCTCAAAACCTAGCGAAAGGATCTGGCGGTGCTCTGTACAGCACTGAC 711

Qy        186 ------------------------------------------------------------ 186
Db        712 AACTGTTCGATTACAGATAACTTTCAAGTGATCTTTGACGGCAATAGTGCTTGGGAAGCC 771

Qy        186 ------------------------------------------------------------ 186
Db        772 GCTCAAGCTCAGGGCGGGGCTATTTGTTGCACTACGACAGATAAAACAGTGACTCTTACT 831

Qy        187 ---AsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArgGlyGlyAlaIleHis 205
Db        832 GGGAACAAAAACCTCTCTTTCACAAATAATACAGCATTGACATATGGCGGAGCCATCTCT 891

Qy        206 ThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaPro 225
Db        892 GGACTCAAGGTCAGTATTTCCGCTGGAGGTCCTACTCTATTTCAAAGTAATATCTCAGGA 951

Qy        226 ThrAlaAlaGlyLys------GlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSer 243
Db        952 AGTAGCGCCGGTCAGGGAGGAGGAGGAGCGATCAATATAGCATCTGCTGGGGAACTCGCT 1011

Qy        244 IleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAlaThrGlyThr 263
Db       1012 CTCTCTGCTACTTCTGGAGATATTACCTTCAATAACAACCAAGTCACCAACGGAAGCACA 1071

Qy        264 ValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAla 283
Db       1072 AGTACAAGAAACGCAATAAATATCATTGATACCGCTAAAGTCACATCGATACGAGCTGCT 1131

Qy        284 GlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGlySerThrSerValAla 303
Db       1132 ACGGGGCAATCTATCTATTTCTATGATCCCATCACAAATCCAGGAACCGCAGCTTCTACC 1191

Qy        304 AspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGluTyrThrGlyThrIle 323
Db       1192 GACACATTGAACTTAAACTTAGCAGATGCGAACAGTGAGATCGAGTATGGGGGTGCGATT 1251

Qy        324 ValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSer 343
Db       1252 GTCTTTTCTGGAGAAAAGCTTTCCCCTACAGAAAAAGCAATCGCTGCAAACGTCACCTCT 1311

Qy        344 LysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspValVal 363
Db       1312 ACTATCCGACAACCTGCAGTATTAGCGCGGGGAGATCTTGTACTTCGTGATGGAGTCACC 1371

Qy        364 LeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThr 383
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Db       1372 GTAACTTTCAAGGATCTGACTCAAAGTCCAGGATCCCGCATCTTAATGGATGGGGGGACT 1431

Qy        384 SerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSer 403

Db       1432 ACACTTAGTGCTAAAGAGGCAAATCTTTCGCTTAATGGCTTAGCAGTAAATCTCTCCTCT 1491

Qy        404 LeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArgIle 423

Db       1492 TTAGATGGAACCAACAAGGCAGCTTTAAAAACAGAAGCTGCAGATAAAAATATCAGCCTA 1551

Qy        424 AspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeuAsn 443

Db       1552 TCGGGAACGATTGCGCTTATTGACACGGAAGGGTCATTCTATGAGAATCATAACTTAAAA 1611

Qy        444 GluAspHisSerTyrAspGlyIleLeuGluLeu---AspAlaGlyLysAspIleValIle 462

Db       1612 AGTGCTAGTACCTATCCT---CTTCTTGAACTTACCACCGCAGGAGCCAACGGAACGATT 1668

Qy        463 SerAlaAspSerArgSerIleAspAlaValGlnSerPro---------TyrGlyTyrGln 479

Db       1669 ACTCTGGGAGCTCTTTCTACCCTGACTCTTCAAGAACCTGAAACCCACTACGGGTATCAA 1728

Qy        480 GlyLysTrpThrIleAsnTrp------SerThrAspAspLysLysAlaThrValSerTrp 497

Db       1729 GGAAACTGGCAGTTGTCTTGGGCAAATGCAACATCCTCAAAAATAGGAAGCATCAACTGG 1788

Qy        498 AlaLysGlnSerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeu 517

Db       1789 ACCCGTACAGGATACATTCCTAGTCCTGAGAGAAAAAGTAATCTCCCTCTAAATAGCTTA 1848

Qy        518 TrpGlySerPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGly 537

Db       1849 TGGGGAAACTTTATAGATATACGCTCGATCAATCAGCTTATAGAAACCAAGTCCAGTGGG 1908

Qy        538 AlaProTyrGluLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGly 557

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Qy        558 ArgGluAsnGlnArgLysPheArgHisValSerGlyGlyAlaValValGlyAlaSerThr 577

Db       1969 ATGCCCACCCGCCATGGTTTCCGCCATATCAGCGGGGGTTATGCACTAGGGATCACAGCA 2028

Qy        578 ArgMetProGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLys 597

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Qy        618 AspAlaSerLeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIle 637

Db       2149 ACAGAAGGGCTCTTCGACATCGCCAATTTCCTCTGGGGAAAAGCAACCCGAGCTCCCTGG 2208

Qy        638 LeuLeuProTyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGly 657

Db       2209 GTGCTCTCTGAGATCTCCCAGATCATTCCTTTATCGTTCGATGCTAAATTCAGTTATCTC 2268

Qy        658 HisThrAspHisArgMetLysThrGluSerLeuProProProProProThrLeuSerThr 677

Db       2269 CATACAGACAACCACATGAAG-------------------------ACATATTATACC 2301

Qy        678 AspHisThr-----------SerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThr 693

Db       2302 GATAACTCTATCATCAAGGGTTCTTGGAGAAACGATGCCTTCTGTGCAGATCTTGGAGCT 2361

Qy        694 ArgValAlaValGluAsnThrSerGlyArgGlyPhePheGlnGluTyrThrProPheVal 713

Db       2362 AGCCTGCCTTTTGTT---ATTTCCGTTCCGTATCTTCTGAAAGAAGTCGAACCTTTTGTC 2418

Qy        714 LysValGlnAlaValTyrAlaArgGlnAspSerPheValGluLeuGlyAlaIleSerArg 733

Db       2419 AAAGTACAGTATATCTATGCGCATCAGCAAGACTTCTACGAGCGTCATGCTGAAGGACGC 2478

Qy        734 AspPheSerAspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLys 753

Db       2479 GCTTTCAATAAAAGCGAGCTTATCAACGTAGAGATTCCTATAGGCGTCACCTTCGAAAGA 2538

Qy        754 ------ArgPheAlaGluGlnTyrTyrHisValValAlaMetTyrSerProAspValCys 771

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Qy        772 ArgSerAsnProLysCysThrThrThrLeuLeuSerAsnGlnGlySerTrpLysThrLys 791

Db       2599 CGACGCAATCCTAAATGTCAAACTTCCCTAATAGCTAGCGATGCTAACTGGATGGCCTAT 2658

Qy        792 GlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGly 811

Db       2659 GGTACCAACCTCGCACGACAAGGTTTTTCTGTTCGTGCTGCGAACCATTTCCAAGTGAAC 2718

Qy        812 AlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArgSerTyr 831

Db       2719 CCCCACATGGAAATCTTCGGTCAATTCGCTTTTGAAGTACGAAGTTCTTCACGAAATTAT 2778

Qy        832 AsnValAspAlaGlySerLysIleLysPhe 841

Db       2779 AATACAAACCTAGGCTCTAAGTTTTGTTTC 2808

RESULT 13
US-09-452-380-1
; Sequence 1, Application US/09452380
; Patent No. US20020094340A1
; GENERAL INFORMATION:
;  APPLICANT:  MURDIN, Andrew D.
;  APPLICANT:  OOMEN, Raymond P.
;  APPLICANT:  WANG, Joe
;  APPLICANT:  DUNN, Pamela
;  TITLE OF INVENTION:  CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE:  032931/0216
;  CURRENT APPLICATION NUMBER: US/09/452,380
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER:  US 60/132,272
;  PRIOR FILING DATE:  1999-05-03
;  PRIOR APPLICATION NUMBER:  US 60/113,439
;  PRIOR FILING DATE:  1998-12-01
;  NUMBER OF SEQ ID NOS:  6
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 3050
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (101)..(2908)
US-09-452-380-1

Alignment Scores:
Pred. No.:              1.68e-126       Length:         3050
Score:                  1335.50         Matches:        311
Percent Similarity:     49.26%          Conservative:   157
Best Local Similarity:  32.74%          Mismatches:     359
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DB:                     9               Gaps:           14

US-09-830-446-27 (1-841) x US-09-452-380-1 (1-3050)

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Qy         21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40

Db        161 ATAGTCGCGGCAGAGGTGACCTTAGAT---AGCAGCAATAATAGCTATGATGGATCTAAC 217

Qy         41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
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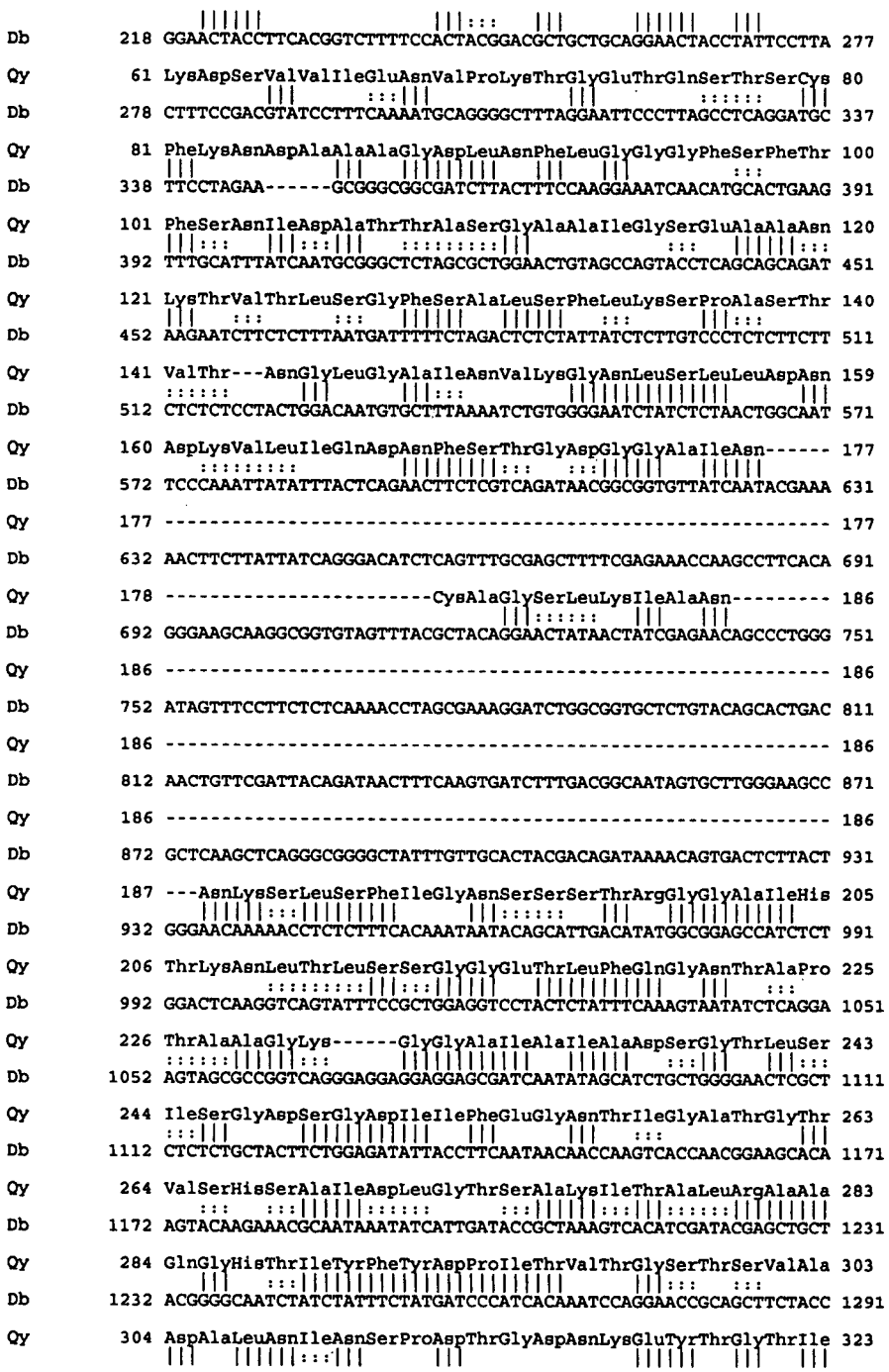
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Qy 61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCys 80
Db 278 CTTTCCGACGTATCCTTTCAAAATGCAGGGGCTTTAGGAATTCCCTTAGCCTCAGGATGC 337
Qy 81 PheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr 100
Db 338 TTCCTAGAA------GCGGGCGGCGATCTTACTTTCCAAGGAAATCAACATGCACTGAAG 391
Qy 101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsn 120
Db 392 TTTGCATTTATCAATGCGGGCTCTAGCGCTGGAACTGTAGCCAGTACCTCAGCAGCAGAT 451
Qy 121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
Db 452 AAGAATCTTCTCTTTAATGATTTTTCTAGACTCTCTATTATCTCTTGTCCCTCTCTTCTT 511
Qy 141 ValThr---AsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsn 159
Db 512 CTCTCTCCTACTGGACAATGTGCTTTAAAATCTGTGGGGAATCTATCTCTAACTGGCAAT 571
Qy 160 AspLysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsn------ 177
Db 572 TCCCAAATTATATTTACTCAGAACTTCTCGTCAGATAACGGCGGTGTTATCAATACGAAA 631
Qy 177 -- 177
Db 632 AACTTCTTATTATCAGGGACATCTCAGTTTGCGAGCTTTTCGAGAAACCAAGCCTTCACA 691
Qy 178 ----------------------CysAlaGlySerLeuLysIleAlaAsn--------- 186
Db 692 GGGAAGCAAGGCGGTGTAGTTTACGCTACAGGAACTATAACTATCGAGAACAGCCCTGGG 751
Qy 186 -- 186
Db 752 ATAGTTTCCTTCTCTCAAAACCTAGCGAAAGGATCTGGCGGTGCTCTGTACAGCACTGAC 811
Qy 186 -- 186
Db 812 AACTGTTCGATTACAGATAACTTTCAAGTGATCTTTGACGGCAATAGTGCTTGGGAAGCC 871
Qy 186 -- 186
Db 872 GCTCAAGCTCAGGGCGGGGCTATTTGTTGCACTACGACAGATAAAACAGTGACTCTTACT 931
Qy 187 ---AsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArgGlyGlyAlaIleHis 205
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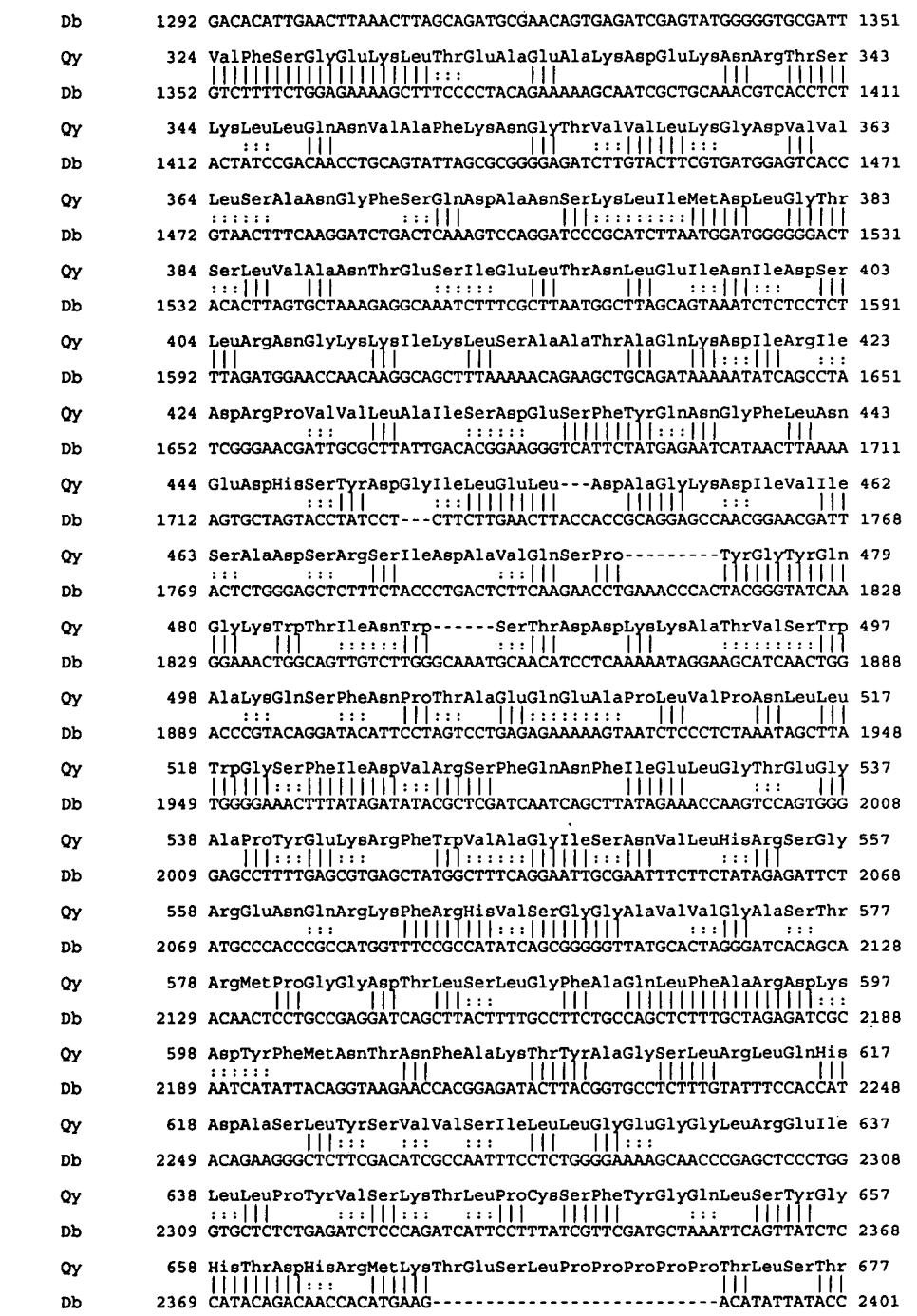
Qy 206 ThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaPro 225
Db 992 GGACTCAAGGTCAGTATTTCCGCTGGAGGTCCTACTCTATTTCAAAGTAATATCTCAGGA 1051
Qy 226 ThrAlaAlaGlyLys------GlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSer 243
Db 1052 AGTAGCGCCGGTCAGGGAGGAGGAGGAGCGATCAATATAGCATCTGCTGGGGAACTCGCT 1111
Qy 244 IleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAlaThrGlyThr 263
Db 1112 CTCTCTGCTACTTCTGGAGATATTACCTTCAATAACAACCAAGTCACCAACGGAAGCACA 1171
Qy 264 ValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAla 283
Db 1172 AGTACAAGAAACGCAATAAATATCATTGATACCGCTAAAGTCACATCGATACGAGCTGCT 1231
Qy 284 GlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGlySerThrSerValAla 303
Db 1232 ACGGGGCAATCTATCTATTTCTATGATCCCATCACAAATCCAGGAACCGCAGCTTCTACC 1291
Qy 304 AspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGluTyrThrGlyThrIle 323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Qy 324 ValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSer 343
Db 1352 GTCTTTTCTGGAGAAAAGCTTTCCCCTACAGAAAAAGCAATCGCTGCAAACGTCACCTCT 1411
Qy 344 LysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspValVal 363
Db 1412 ACTATCCGACAACCTGCAGTATTAGCGCGGGGAGATCTTGTACTTCGTGATGGAGTCACC 1471
Qy 364 LeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThr 383
Db 1472 GTAACTTTCAAGGATCTGACTCAAAGTCCAGGATCCCGCATCTTAATGGATGGGGGGACT 1531
Qy 384 SerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSer 403
Db 1532 ACACTTAGTGCTAAAGAGGCAAATCTTTCGCTTAATGGCTTAGCAGTAAATCTCTCCTCT 1591
Qy 404 LeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArgIle 423
Db 1592 TTAGATGGAACCAACAAGGCAGCTTTAAAAACAGAAGCTGCAGATAAAAATATCAGCCTA 1651
Qy 424 AspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeuAsn 443
Db 1652 TCGGGAACGATTGCGCTTATTGACACGGAAGGGTCATTCTATGAGAATCATAACTTAAAA 1711
Qy 444 GluAspHisSerTyrAspGlyIleLeuGluLeu---AspAlaGlyLysAspIleValIle 462
Db 1712 AGTGCTAGTACCTATCCT---CTTCTTGAACTTACCACCGCAGGAGCCAACGGAACGATT 1768
Qy 463 SerAlaAspSerArgSerIleAspAlaValGlnSerPro---------TyrGlyTyrGln 479
Db 1769 ACTCTGGGAGCTCTTTCTACCCTGACTCTTCAAGAACCTGAAACCCACTACGGGTATCAA 1828
Qy 480 GlyLysTrpThrIleAsnTrp------SerThrAspAspLysLysAlaThrValSerTrp 497
Db 1829 GGAAACTGGCAGTTGTCTTGGGCAAATGCAACATCCTCAAAAATAGGAAGCATCAACTGG 1888
Qy 498 AlaLysGlnSerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeu 517
Db 1889 ACCCGTACAGGATACATTCCTAGTCCTGAGAGAAAAAGTAATCTCCCTCTAAATAGCTTA 1948
Qy 518 TrpGlySerPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGly 537
Db 1949 TGGGGAAACTTTATAGATATACGCTCGATCAATCAGCTTATAGAAACCAAGTCCAGTGGG 2008
Qy 538 AlaProTyrGluLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGly 557
Db 2009 GAGCCTTTTGAGCGTGAGCTATGGCTTTCAGGAATTGCGAATTTCTTCTATAGAGATTCT 2068
Qy 558 ArgGluAsnGlnArgLysPheArgHisValSerGlyGlyAlaValValGlyAlaSerThr 577
Db 2069 ATGCCCACCCGCCATGGTTTCCGCCATATCAGCGGGGGTTATGCACTAGGGATCACAGCA 2128
Qy 578 ArgMetProGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLys 597
Db 2129 ACAACTCCTGCCGAGGATCAGCTTACTTTTGCCTTCTGCCAGCTCTTTGCTAGAGATCGC 2188
Qy 598 AspTyrPheMetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHis 617
Db 2189 AATCATATTACAGGTAAGAACCACGGAGATACTTACGGTGCCTCTTTGTATTTCCACCAT 2248
Qy 618 AspAlaSerLeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIle 637
Db 2249 ACAGAAGGGCTCTTCGACATCGCCAATTTCCTCTGGGGAAAAGCAACCCGAGCTCCCTGG 2308
Qy 638 LeuLeuProTyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGly 657
Db 2309 GTGCTCTCTGAGATCTCCCAGATCATTCCTTTATCGTTCGATGCTAAATTCAGTTATCTC 2368
Qy 658 HisThrAspHisArgMetLysThrGluSerLeuProProProProProThrLeuSerThr 677
Db 2369 CATACAGACAACCACATGAAG----------ACATATTATACC 2401

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Qy       678 AspHisThr----------SerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThr 693
Db      2402 GATAACTCTATCATCAAGGGTTCTTGGAGAAACGATGCCTTCTGTGCAGATCTTGGAGCT 2461

Qy       694 ArgValAlaValGluAsnThrSerGlyArgGlyPhePheGlnGluTyrThrProPheVal 713
Db      2462 AGCCTGCCTTTTGTT---ATTTCCGTTCCGTATCTTCTGAAAGAAGTCGAACCTTTTGTC 2518

Qy       714 LysValGlnAlaValTyrAlaArgGlnAspSerPheValGluLeuGlyAlaIleSerArg 733
Db      2519 AAAGTACAGTATATCTATGCGCATCAGCAAGACTTCTACGAGCGTCATGCTGAAGGACGC 2578

Qy       734 AspPheSerAspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLys 753
Db      2579 GCTTTCAATAAAAGCGAGCTTATCAACGTAGAGATTCCTATAGGCGTCACCTTCGAAAGA 2638

Qy       754 ------ArgPheAlaGluGlnTyrTyrHisValValAlaMetTyrSerProAspValCys 771
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Qy       772 ArgSerAsnProLysCysThrThrThrLeuLeuSerAsnGlnGlySerTrpLysThrLys 791
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Qy       812 AlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArgSerTyr 831
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RESULT 14
US-10-324-129-1
; Sequence 1, Application US/10324129
; Publication No. US20030157124A1
; GENERAL INFORMATION:
; APPLICANT: Murdin et al.
; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses there
; FILE REFERENCE: 77813-4
; CURRENT APPLICATION NUMBER: US/10/324,129
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/113,439
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/132,272
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3050
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(2908)
US-10-324-129-1

Alignment Scores:

Pred. No.:	1.68e-126	Length:	3050
Score:	1335.50	Matches:	311
Percent Similarity:	49.26%	Conservative:	157
Best Local Similarity:	32.74%	Mismatches:	359
Query Match:	31.09%	Indels:	123
DB:	13	Gaps:	14

US-09-830-446-27 (1-841) x US-10-324-129-1 (1-3050)

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Qy         1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20

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Qy        21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
Db       161 ATAGTCGCGGCAGAGGTGACCTTAGAT---AGCAGCAATAATAGCTATGATGGATCTAAC 217

Qy        41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
Db       218 GGAACTACCTTCACGGTCTTTTCCACTACGGACGCTGCTGCAGGAACTACCTATTCCTTA 277

Qy        61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCys 80
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Qy       101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsn 120
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Qy       121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
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Qy       141 ValThr---AsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsn 159
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Db       872 GCTCAAGCTCAGGGCGGGGCTATTTGTTGCACTACGACAGATAAAACAGTGACTCTTACT 931

Qy       187 ---AsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArgGlyGlyAlaIleHis 205
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Qy       206 ThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaPro 225
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Qy       226 ThrAlaAlaGlyLys------GlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSer 243
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Qy        364 LeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThr 383

Db       1472 GTAACTTTCAAGGATCTGACTCAAAGTCCAGGATCCCGCATCTTAATGGATGGGGGGACT 1531

Qy        384 SerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSer 403

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Db       1769 ACTCTGGGAGCTCTTTCTACCCTGACTCTTCAAGAACCTGAAACCCACTACGGGTATCAA 1828

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Qy        538 AlaProTyrGluLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGly 557

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Db       2129 ACAACTCCTGCCGAGGATCAGCTTACTTTTGCCTTCTGCCAGCTCTTTGCTAGAGATCGC 2188

Qy        598 AspTyrPheMetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHis 617

Db       2189 AATCATATTACAGGTAAGAACCACGGAGATACTTACGGTGCCTCTTTGTATTTCCACCAT 2248

Qy        618 AspAlaSerLeuTyrSerValValSerIleLeuGluGlyGluGlyGlyLeuArgGluIle 637

Db       2249 ACAGAAGGGCTCTTCGACATCGCCAATTTCCTCTGGGGAAAAGCAACCCGAGCTCCCTGG 2308

Qy        638 LeuLeuProTyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGly 657

Db       2309 GTGCTCTCTGAGATCTCCCAGATCATTCCTTTATCGTTCGATGCTAAATTCAGTTATCTC 2368

Qy        658 HisThrAspHisArgMetLysThrGluSerLeuProProProProProThrLeuSerThr 677

Db       2369 CATACAGACAACCACATGAAG-------------------------ACATATTATACC 2401

Qy        678 AspHisThr-----------SerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThr 693

Db       2402 GATAACTCTATCATCAAGGGTTCTTGGAGAAACGATGCCTTCTGTGCAGATCTTGGAGCT 2461

Qy        694 ArgValAlaValGluAsnThrSerGlyArgGlyPhePheGlnGluTyrThrProPheVal 713

Db       2462 AGCCTGCCTTTTGTT---ATTTCCGTTCCGTATCTTCTGAAAGAAGTCGAACCTTTTGTC 2518

Qy        714 LysValGlnAlaValTyrAlaArgGlnAspSerPheValGluLeuGlyAlaIleSerArg 733

Db       2519 AAAGTACAGTATATCTATGCGCATCAGCAAGACTTCTACGAGCGTCATGCTGAAGGACGC 2578

Qy        734 AspPheSerAspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLys 753

Db       2579 GCTTTCAATAAAAGCGAGCTTATCAACGTAGAGATTCCTATAGGCGTCACCTTCGAAAGA 2638

Qy        754 ------ArgPheAlaGluGlnTyrTyrHisValValAlaMetTyrSerProAspValCys 771

Db       2639 GACTCAAAATCAGAAAAGGGAACTTACGATCTTACTCTTATGTATATACTCGATGCTTAC 2698

Qy        772 ArgSerAsnProLysCysThrThrThrLeuLeuSerAsnGlnGlySerTrpLysThrLys 791

Db       2699 CGACGCAATCCTAAATGTCAAACTTCCCTAATAGCTAGCGATGCTAACTGGATGGCCTAT 2758

Qy        792 GlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGly 811

Db       2759 GGTACCAACCTCGCACGACAAGGTTTTTCTGTTCGTGCTGCGAACCATTTCCAAGTGAAC 2818

Qy        812 AlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArgSerTyr 831

Db       2819 CCCCACATGGAAATCTTCGGTCAATTCGCTTTTGAAGTACGAAGTTCTTCACGAAATTAT 2878

Qy        832 AsnValAspAlaGlySerLysIleLysPhe 841

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RESULT 15
US-09-738-269-56
; Sequence 56, Application US/09738269
; Publication No. US20030185848A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEMKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
; TITLE OF INVENTION: NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
; TITLE OF INVENTION: CHLAMYDIA PSITTACI
; FILE REFERENCE: UTSD:659
; CURRENT APPLICATION NUMBER: US/09/738,269
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 2781
; TYPE: DNA
; ORGANISM: Chlamydia psittaci
US-09-738-269-56

Alignment Scores:

Pred. No.:	1.58e-121	Length:	2781
Score:	1286.50	Matches:	327
Percent Similarity:	47.49%	Conservative:	127
Best Local Similarity:	34.21%	Mismatches:	357

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Query Match:          29.95%      Indels:       145
DB:                   13          Gaps:          17

US-09-830-446-27 (1-841) x US-09-738-269-56 (1-2781)

Qy          1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSer--- 19
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Db          1 ATGAGGCCTTCTTTATATAAGATTTTAATATCGTCGACGCTGACGTTACCAATATCTTTT 60

Qy         20 --------------AsnLeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsn 34
                           :::          |||  |||  |||   :::      :::|||
Db         61 CACTTCTCGCAATTGCATGCAGAAGTGGCTTTAACTCAAGAATCTATTCTCGATGCAAAT 120

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Qy         75 ThrGlnSerThrSerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGly 94
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Db        217 CTTGCTTCCTCAGCTTTTGTTCAG---------ACTGCAGACAACCTAACTTTCAAAGGG 267

Qy         95 GlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIle 114
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Qy        155 SerLeuLeuAspAsnAspLysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGly 174
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Qy        175 AlaIleAsnCys---------------------------------------------- 178
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Qy        178 ---------------------------------------------------------- 178

Db        685 TCAGAAGCTTCTATGACGATTGCAGGTAACAACCACGTTGCTTTTAGCAACAATGCTGTT 744

Qy        179 ----------------------------------------------------------AlaGly 180
                                                                       |||
Db        745 TCCGGTTCATCTGATGGTTGCGGTGGAGCTATCCATTGTAGCAAAACAGGTTCAGCACCG 804

Qy        181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArg 200
              :::|||   |||   :::|||||   |||   |||       |||:::||||||   :::
Db        805 ACCCTTACTATAAGAGATAACAAAGTCTTGATTTTTGAGGAAAATACTTCTTCAGCAAAA 864

Qy        201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220
              ||||||||||||:::|||      |||   |||:::|||||||||   |||   |||
Db        865 GGTGGAGCGATTTACACCGATAAACTCATATTGACTTCTGGTGGGCCTACGGCATTTATC 924

Qy        221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240
                 |||          |||      ||||||||||||||||   ||||||   :::|||
Db        925 AATAACAAAGTTACCCATGCTACACCTAAGGGTGGAGCTATTGGTATTGCTGCCAATGGA 984

Qy        241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260
              |||::::::   :::   |||||||||   |||:::   |||   :::
Db        985 GAATGTAGCTTAACCGCTGAACATGGGGATATTACTTTTGATAATAACCTGATGGCCACA 1044

Qy        261 ------ThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThr 278
                    |||:::      :::||||||::::::       :::   |||
Db       1045 CAAGACAATGCTACAATAAAAAGAAATGCCATTAACATTGAAGGCAATGGTAAATTCGTC 1104

Qy        279 AlaLeuArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGly 298
              |||||||||||||   |||  ||||||  ||||||||||||||||||||   |||
Db       1105 AACTTACGTGCAGCGTCTGGAAAGACGATTTCTTTCTATGATCCTATCACAGTTGAAGGT 1164

Qy        299 SerThrSerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGlu 318
                 :::   ||||||   |||   :::|||       :::   ||||||   |||
Db       1165 ------AATGCTGCTGATCTTCTCACTTTGAATAAAGCTGAG---GGTGAT---AAAACG 1212

Qy        319 TyrThrGlyThrIleValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGlu 338
              |||   |||   |||:::|||||||||||||||||||||||||   :::|||
Db       1213 TATAATGGAAGAATTATTTTTTCAGGAGAAAAGCTCACTGAAGAACAAGCTGCTGTTGCG 1272

Qy        339 LysAsnArgThrSerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeu 358
              |||       :::          |||   :::              |||   :::|||||||
Db       1273 GATAACCTAAAGACAACATTTACACAGCCTATCACTTTAGCTGCTGGTGAACTTGTGTTA 1332

Qy        359 LysGlyAspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIle 378
              :::       |||   :::   |||              |||   |||   |||   ::::::
Db       1333 CGCAGCGGTGTGGAAGTAGAAGCAAAAACAGTCGTGCAAACAGCAGGATCTTTGATTCTG 1392

Qy        379 MetAspLeuGlyThrSerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGlu 398
              ||||||   ||||||   |||   |||   ||||||          ||||||||||||
Db       1393 ATGGATGCAGGCACAAAGTTATCCGCAAAAACAGAAGATGCTACACTGACGAATCTGGCT 1452

Qy        399 IleAsnIleAspSerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGln 418
              ||||||   ::::::|||          |||          :::   |||   |||
Db       1453 ATTAATCCGAATACCTTAGATGGGAAAAAATTCGCCGTAGTCGATGCCGTTGCTGCTGGG 1512

Qy        419 LysAspIleArgIleAspArgProValValLeuAlaIleSerAspGluSerPheTyrGln 438
              |||::::::   :::          :::   :::                  ||||||:::
Db       1513 AAGAATGTGACTTTATCAGGTGCTATTGGCGTTATTGATCCTACAGGGAAGTTTTATGAA 1572

Qy        439 AsnGlyPheLeuAsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLys 458
              |||       ||||||:::       :::       ||||||                |||
Db       1573 AACCATAAGCTAAATGATACGTTAGCTTTAGGAGGAATTCAACTTTCTGGGAAAGGTTCG 1632

Qy        459 AspIleValIleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyr 478
                    :::       |||       :::          ::::::   |||||||||
Db       1633 GTGACAACAACCAACGTGCCTAGTCATGTTGTTGGTGTTGCTGAAACCCACTATGGTTAT 1692

Qy        479 GlnGlyLysTrpThrIleAsnTrpSerThrAspAsp-----------------LysLys 492
              ||||||   |||:::::::::|||      |||:::                  :::
Db       1693 CAAGGAAACTGGTCTGTCAGTTGGGTCAAAGATAATAACTCTGATCCTAAAACACAAACA 1752

Qy        493 AlaThrValSerTrpAlaLysGlnSerPheAsnProThrAlaGluGlnGluAlaProLeu 512
              |||       :::|||   |||       :::   |||       |||:::   |||||||||
Db       1753 GCAATCTTTACCTGGAATAAAACAGGATATGTTCCAAATCCTGAACGTCGTGCTCCGCTA 1812

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Db       1813 GTACTCAATAGCCTTTGGGGATCCTTTATAGATTTACGTTCTATTCAAGATGTCTTGGAA 1872

Qy        533 LeuGlyThrGluGlyAlaProTyrGluLysArg---PheTrpValAlaGlyIleSerAsn 551
                    :::                 :::|||      ||||||:::|||||   |||
Db       1873 CGTAGTGTTGATAGTATTCTTGAGACACGTCGTGGTTTGTGGGTCTCTGGAATTGGGAAC 1932

Qy        552 ValLeuHisArgSerGlyArgGluAsnGlnArgLysPheArgHisValSerGlyGlyAla 571
              |||:::                 ||||||||||||||||:::|||   |||
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Qy        572 ValValGlyAlaSerThrArgMetProGlyGlyAspThrLeuSerLeuGlyPheAlaGln 591
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Qy        592 LeuPheAlaArgAspLysAspTyrPheMetAsnThrAsnPheAlaLysThrTyrAlaGly 611
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Db       2053 TTATTTGCAAAAGATAAAGACTACCTTGTAAGCAAGAACGCCGCAAACGTCTATGCGGGT 2112

Qy        612 SerLeuArgLeuGlnHisAspAlaSerLeuTyrSerValValSerIleLeuLeuGlyGlu 631
Db       2113 TCTGTATATTATCAGCATGTGAGCAAGTTTGATGATCTCACGCGGTTATTTAATGGGCCT 2172

Qy        632 GlyGlyLeuArgGluIleLeuLeuProTyrValSerLysThrLeuProCysSerPheTyr 651
Db       2173 ------------AACACGTGTTGTTCAGGGTTTTCTAAAGAGATTCCTATTTTCTTGGAT 2220

Qy        652 GlyGlnLeuSerTyrGlyHisThrAspHisArgMetLysThrGluSerLeuProProPro 671
Db       2221 GCACAAATTACCTATTGCCACACGGCCAACAACATGACAACGTCC-------------- 2265

Qy        672 ProProThrLeuSerThrAspHisThr------------SerTrpGlyGlyTyrValTrp 687
Db       2266 ------------TATACAGACTATCCTGAAGTGAAAGGTTCTTGGGGTAATGATACCCTG 2313

Qy        688 AlaGlyGluLeuGlyThrArgValAlaValGluAsnThrSerGlyArgGlyPhePheGln 707
Db       2314 GGCTTAACTTTGTCTACTAGCGTACCTATCCCGGTATTTAGTTCT---TCTATCTTTGAT 2370

Qy        708 GluTyrThrProPheValLysValGlnAlaValTyrAlaArgGlnAspSerPheValGlu 727
Db       2371 AGTTATGCACCGTTTGCAAAATTACAAGTTGTCTATGCGCACCAAGATGACTTTAAAGAA 2430

Qy        728 LeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyrAsnLeuAlaIleProLeu 747
Db       2431 CCAACAACAGAAGGCCGGGTCTTTGAAAGCAGCGATCTTCTCAACGTTTCTGTACCTATA 2490

Qy        748 GlyIleLysLeuGluLys---ArgPheAlaGluGln---TyrTyrHisValValAlaMet 765
Db       2491 GGTATAAAATTTGAGAAACTCTCCTATGGAGAGAGAAGTGCTTATGATCTTACACTGATG 2550

Qy        766 TyrSerProAspValCysArgSerAsnProLysCysThrThrThrLeuLeuSerAsnGln 785
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Qy        806 GlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTrpArg 825
Db       2671 AACCATATTGCCTTAACCTCTGGTGTTGAGATGTTCAGTCAGTTTGGTTTCGAATTACGA 2730

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Search completed: January 29, 2004, 18:26:27
Job time : 2187 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 29, 2004, 10:21:11 ; Search time 7888 Seconds
(without alignments)
4361.688 Million cell updates/sec

Title: US-09-830-446-27
Perfect score: 4295
Sequence: 1 MKIPLRFLLISLVPTLSMSN.....FEWRGSSRSYNVDAGSKIKF 841

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US09830446/runat_29012004_102102_19204/app_query.fasta_1.1031
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	4295	100.0	2526	6	AX349617	AX349617 Sequence
	2	4295	100.0	10574	1	AE001586	AE001586 Chlamydia
c	3	4295	100.0	12127	1	AE002235	AE002235 Chlamydop
	4	4295	100.0	26920	1	CPN133035	AJ133035 Chlamydia
	5	4278	99.6	2526	6	A81833	A81833 Sequence 7
	6	4260	99.2	299650	1	AP002545	AP002545 Chlamydop
	7	4255	99.1	110000	6	AR310754_00	AR310754 Sequence
	8	2603	60.6	1830	6	A81855	A81855 Sequence 29
	9	1569.5	36.5	2787	6	A81835	A81835 Sequence 9
	10	1558.5	36.3	16448	1	AE001587	AE001587 Chlamydia
	11	1497	34.9	2520	6	AX662085	AX662085 Sequence
	12	1497	34.9	2520	6	AX666157	AX666157 Sequence
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	14	1497	34.9	6234	1	CPU65943	U65943 Chlamydophi
	15	1435.5	33.4	2787	6	AX349593	AX349593 Sequence
	16	1435.5	33.4	3200	6	A81827	A81827 Sequence 1
	17	1435.5	33.4	6030	1	CPOMP54	AJ001311 Chlamydia
	18	1435.5	33.4	10757	1	AE001628	AE001628 Chlamydia
c	19	1435.5	33.4	12676	1	AE002192	AE002192 Chlamydop
	20	1435.5	33.4	17280	1	CPN133034	AJ133034 Chlamydia
	21	1435.5	33.4	110000	6	AR310754_05	Continuation (6 of
	22	1435.5	33.4	300650	1	AP002546	AP002546 Chlamydop
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	26	1407.5	32.8	2787	6	AX349573	AX349573 Sequence
	27	1406.5	32.7	2793	6	A81841	A81841 Sequence 15
	28	1406.5	32.7	2815	6	A81829	A81829 Sequence 3
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	39	1359.5	31.7	3000	6	A81851	A81851 Sequence 25
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	41	1357.5	31.6	2241	6	AX349497	AX349497 Sequence
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ALIGNMENTS

RESULT 1

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LOCUS       AX349617               2526 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 140 from Patent WO0202606.
ACCESSION   AX349617
VERSION     AX349617.1  GI:18615415
KEYWORDS    .
SOURCE      Chlamydophila pneumoniae
  ORGANISM  Chlamydophila pneumoniae
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
REFERENCE   1
  AUTHORS   Ratti,G. and Grandi,G.
  TITLE     Immunisation against Chlamydia pneumoniae
  JOURNAL   Patent: WO 0202606-A 140 10-JAN-2002;
            Chiron S.p.A. (IT)
FEATURES             Location/Qualifiers
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                     /organism="Chlamydophila pneumoniae"
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                     /db_xref="taxon:83558"
BASE COUNT      693 a    493 c    601 g    739 t
ORIGIN

Alignment Scores:
Pred. No.:              1.11e-255      Length:         2526
Score:                  4295.00        Matches:        841
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     6              Gaps:           0

US-09-830-446-27 (1-841) x AX349617 (1-2526)

Qy          1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
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Db          1 ATGAAGATTCCACTCCGCTTTTTATTGATATCATTAGTACCTACGCTTTCTATGTCGAAT 60

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ACCESSION   AE001586 AE001363
VERSION     AE001586.1  GI:4376263
KEYWORDS    .
SOURCE      Chlamydophila pneumoniae CWL029
  ORGANISM  Chlamydophila pneumoniae CWL029
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
REFERENCE   1  (bases 1 to 10574)
  AUTHORS   Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Hyman,R.W.,
            Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S.
  TITLE     Comparative genomes of Chlamydia pneumoniae and C. trachomatis
  JOURNAL   Nat. Genet. 21 (4), 385-389 (1999)
  MEDLINE   99206606
   PUBMED   10192388
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            Grimwood,J., Davis,R.W. and Stephens,R.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-DEC-1998) Program in Infectious Diseases, University
            of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA
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ORIGIN

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Score:                  4295.00         Matches:        841
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     1               Gaps:           0
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US-09-830-446-27 (1-841) x AE001586 (1-10574)

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Db       8058 AAAGATTCTGTAGTTATAGAAAATGTACCCAAAACAGGGGAAACTCAGTCTACTAGTTGT 8117

Qy         81 PheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr 100
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Db       8118 TTTAAAAATGACGCTGCAGCTGGAGATCTAAATTTCTTAGGAGGGGGATTTTCTTTCACA 8177

Qy        101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsn 120
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Db       8178 TTTAGCAATATCGATGCAACCACGGCTTCTGGAGCTGCTATTGGAAGTGAAGCAGCTAAT 8237

Qy        121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
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Db       8238 AAGACAGTCACGTTATCAGGATTTTCGGCACTTTCTTTTCTTAAATCCCCAGCAAGTACA 8297

Qy        141 ValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAsp 160
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Db       8298 GTGACTAATGGATTGGGAGCTATCAATGTTAAAGGGAATTTAAGCCTATTGGATAATGAT 8357

Qy        161 LysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180
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Db       8358 AAGGTATTGATTCAGGACAATTTCTCAACAGGAGATGGCGGAGCAATTAATTGTGCAGGC 8417

Qy        181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArg 200
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Db       8418 TCCTTGAAGATCGCAAACAATAAGTCCCTTTCTTTTATTGGAAATAGTTCTTCAACACGT 8477

Qy        201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220
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Qy        221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240
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Db       8538 GGGAATACAGCGCCTACGGCTGCTGGTAAAGGAGGTGCTATCGCGATTGCAGACTCTGGC 8597

Qy        241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260
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Db       8598 ACCCTATCCATTTCTGGAGACAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCT 8657

Qy        261 ThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeu 280
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Db       8658 ACAGGAACCGTCTCTCATAGTGCTATTGATTTAGGAACTAGCGCTAAGATAACTGCGTTA 8717

Qy        281 ArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGlySerThr 300
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Db       8718 CGTGCTGCGCAAGGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGACA 8777

Qy        301 SerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGluTyrThr 320
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Db       8838 GGAACCATAGTCTTTTCTGGAGAGAAGCTCACGGAGGCAGAAGCTAAAGATGAGAAGAAC 8897

Qy        341 ArgThrSerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLysGly 360
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Qy        381 LeuGlyThrSerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsn 400
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Db       9018 TTAGGGACGTCGTTGGTTGCAAACACCGAAAGTATCGAGTTAACGAATTTGGAAATTAAT 9077

Qy        401 IleAspSerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAsp 420
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Qy        421 IleArgIleAspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGly 440
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Qy        441 PheLeuAsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIle 460
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Qy        461 ValIleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGly 480
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Db       9258 GTGATTTCTGCAGATTCTCGCAGTATAGATGCTGTACAATCTCCGTATGGCTATCAGGGA 9317

Qy        481 LysTrpThrIleAsnTrpSerThrAspAspLysLysAlaThrValSerTrpAlaLysGln 500
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Qy        501 SerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySer 520
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Qy        521 PheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTyr 540
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Db       9438 TTTATAGATGTTCGTTCCTTCCAGAATTTTATAGAGCTAGGTACTGAAGGTGCTCCTTAC 9497

Qy        541 GluLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAsn 560
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Qy        561 GlnArgLysPheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArgMetPro 580
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Qy        621 LeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuPro 640
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Qy        681 SerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAlaValGluAsnThr 700
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Qy        701 SerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGlnAlaValTyrAla 720
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Db      10038 CGCCAAGATAGCTTTGTAGAACTAGGAGCTATCAGTCGTGATTTTAGTGATTCGCATCTT 10097

Qy        741 TyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPheAlaGluGlnTyrTyr 760
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VERSION     AE002235.2  GI:8163495
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SOURCE      Chlamydophila pneumoniae AR39
  ORGANISM  Chlamydophila pneumoniae AR39
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REFERENCE   1  (bases 1 to 12127)
  AUTHORS   Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F.,
            White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T.,
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            Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J.,
            McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
  TITLE     Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
            pneumoniae AR39
  JOURNAL   Nucleic Acids Res. 28 (6), 1397-1406 (2000)
  MEDLINE   20150255
   PUBMED   10684935
REFERENCE   2  (bases 1 to 12127)
  AUTHORS   Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F.,
            White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T.,
            Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B.,
            Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J.,
            McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAR-2000) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA
COMMENT     On Jun 1, 2000 this sequence version replaced gi:7189672.
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ORIGIN

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Score:                    4295.00        Matches:         841
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       1              Gaps:            0

US-09-830-446-27 (1-841) x AE002235 (1-12127)

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Db      11318 GGCGGAGCGATTCATACCAAAAACCTCACACTATCTTCTGGTGGGGAAACTCTATTTCAG 11259

Qy        221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240
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Qy        241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260
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Qy        301 SerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGluTyrThr 320
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Qy        361 AspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAsp 380
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Qy        441 PheLeuAsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIle 460

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Qy        461 ValIleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGly 480

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Qy        841 Phe 841

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DEFINITION  Chlamydia pneumoniae GGAI-protein family cluster B, genes omp6,
            hb1, hb2, hb3, hb4, hb5, hb6, hb7, omp7, pseudogenes omp8, omp9,
            omp15, strain VR1310.
ACCESSION   AJ133035
VERSION     AJ133035.1  GI:4455890
KEYWORDS    HB1 gene; HB2 gene; hb3 gene; hb4 gene; hb5 gene; hb6 gene; hb7
            gene; omp15 gene; omp6 gene; omp7 gene; omp8 gene; omp9 gene; outer
            membrane protein 6; outer membrane protein 7; pseudogene.
SOURCE      Chlamydophila pneumoniae
  ORGANISM  Chlamydophila pneumoniae
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
REFERENCE   1
  AUTHORS   Daugaard,L., Hjerno,K., Knudsen,K., Madsen,A.S., Christiansen,G.
            and Birkelund,S.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 26920)
  AUTHORS   Boesen,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JAN-1999) Boesen T., Department of Medical
            Microbiology and Immunology, University of Aarhus, The Bartholin
            Building, DK-8000 Aarhus, DENMARK
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Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       1             Gaps:            0

US-09-830-446-27 (1-841) x CPN133035 (1-26920)

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Qy        621 LeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuPro 640
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Qy       741 TyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPheAlaGluGlnTyrTyr 760
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Qy       801 IleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsnPhe 820
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VERSION     A81833.1  GI:6731867
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2526)
  AUTHORS   Madsen,A. and Birkelund,S.
  TITLE     NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA PNEUMONIAE
  JOURNAL   Patent: WO 9858953-A 7 30-DEC-1998;
            MADSEN ANNA SOFIE (DK); BIRKELUND SVEND (DK)
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Percent Similarity:     99.88%          Conservative:   3
Best Local Similarity:  99.52%          Mismatches:     1
Query Match:            99.60%          Indels:         0
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US-09-830-446-27 (1-841) x A81833 (1-2526)
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Qy        21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
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Qy        41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
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Qy        61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCys 80
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Qy       121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
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Qy       141 ValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAsp 160
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Qy       161 LysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180
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REFERENCE   1
  AUTHORS   Shirai,M., Hirakawa,H., Ouchi,K., Tabuchi,M., Kishi,F., Kimoto,M.,
            Takeuchi,A., Nishida,J., Shibata,K., Fujinaga,R., Yoneda,H.,
            Matsushima,H., Tanaka,C., Furukawa,S., Miura,K., Nakazawa,A.,
            Ishii,K., Shiba,T., Hattori,M., Kuhara,S. and Nakazawa,T.
  TITLE     Comparison of outer membrane protein genes omp and pmp in the whole
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            the United States
  JOURNAL   J. Infect. Dis. 181 Suppl 3, S524-S527 (2000)
  MEDLINE   20298986
   PUBMED   10839753
REFERENCE   2
  AUTHORS   Shirai,M., Hirakawa,H., Kimoto,M., Tabuchi,M., Kishi,F., Ouchi,K.,
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  TITLE     Comparison of whole genome sequences of Chlamydia pneumoniae J138
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  JOURNAL   Nucleic Acids Res. 28 (12), 2311-2314 (2000)
  MEDLINE   20330349
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REFERENCE   3  (bases 1 to 299650)
  AUTHORS   Shirai,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUL-2000) Mutsunori Shirai, Yamaguchi University
            School of Medicine, Department of Microbiology; 1-1-1
            Minamikogushi, Ube, Yamaguchi 755-8505, Japan
            (E-mail:mshirai@po.cc.yamaguchi-u.ac.jp, Tel:81-836-22-2227,
            Fax:81-836-22-2415)
COMMENT     On or before Aug 31, 2000 this sequence version replaced
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US-09-830-446-27 (1-841) x AP002545 (1-299650)

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  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
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  JOURNAL   Patent: US 6559294-A 1 06-MAY-2003;
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US-09-830-446-27 (1-841) x AR310754_00 (1-110000)

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Db     30209 TATTCGTATAGATCGTCCTGTTGTACTGGCAATTAGCGATGAGAGTTTTTATCAAAATGG 30268

Qy       440 yPheLeuAsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIl 460
Db     30269 CTTTTTGAATGAGGACCATTCCTATGATGGGATTCTTGAGTTAGATGCTGGGAAAGACAT 30328

Qy       460 eValIleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGl 480
Db     30329 CGTGATTTCTGCAGATTCTCGCAGTATAGATGCTGTACAATCTCCGTATGGCTATCAGGG 30388

Qy       480 yLysTrpThrIleAsnTrpSerThrAspAspLysLysAlaThrValSerTrpAlaLysGl 500
Db     30389 AAAGTGGACGATCAATTGGTCTACTGATGATAAGAAAGCTACGGTTTCTTGGGCGAAGCA 30448

Qy       500 nSerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySe 520
Db     30449 GAGTTTTAATCCCACTGCTGAGCAGGAGGCTCCGTTAGTTCCTAATCTTCTTTGGGGTTC 30508

Qy       520 rPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTy 540
Db     30509 TTTTATAGATGTTCGTTCCTTCCAGAATTTTATAGAGCTAGGTACTGAAGGTGCTCCTTA 30568

Qy       540 rGluLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAs 560
Db     30569 CGAAAAGAGATTTTGGGTTGCAGGCATTTCCAATGTTTTGCATAGGAGCGGTCGTGAAAA 30628

Qy       560 nGlnArgLysPheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArgMetPr 580
Db     30629 TCAAAGGAAATTCCGTCATGTGAGTGGAGGTGCTGTAGTAGGTGCTAGCACGAGGATGCC 30688

Qy       580 oGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPh 600
Db     30689 GGGTGGTGATACCTTGTCTCTGGGTTTGCTCAGCTCTTTGCGCGTGACAAAGACTACTT 30748

Qy       600 eMetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSe 620
Db     30749 TATGAATACCAATTTCGCAAAGACCTACGCAGGATCTTTACGTTTGCAGCACGATGCTTC 30808

Qy       620 rLeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuPr 640
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Db     30809 CCTATACTCTGTGGTGAGTATCCTTTTAGGAGAGGGAGGACTCCGCGAGATCCTGTTGCC 30868

Qy       640 oTyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAs 660
Db     30869 TTATGTTTCCAAGACTCTGCCGTGCTCTTTCTATGGGCAGCTTAGCTACGGCCATACGGA 30928

Qy       660 pHisArgMetLysThrGluSerLeuProProProProProThrLeuSerThrAspHisTh 680
Db     30929 TCATCGCATGAAGACCGAGTCTCTACCCCCCCCCCCCCCGACGCTCTCGACGGATCATAC 30988

Qy       680 rSerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAlaValGluAsnTh 700
Db     30989 TTCTTGGGGAGGATATGTCTGGGCTGGAGAGCTGGGAACTCGAGTTGCTGTTGAAAATAC 31048

Qy       700 rSerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGlnAlaValTyrAl 720
Db     31049 CAGCGGCAGAGGATTTTTCCAAGAGTACACTCCATTTGTAAAAGTCCAAGCTGTTTACGC 31108

Qy       720 aArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSerAspSerHisLe 740
Db     31109 TCGCCAAGATAGCTTTGTAGAACTAGGAGCTATCAGTCGTGATTTTAGTGATTCGCATCT 31168

Qy       740 uTyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPheAlaGluGlnTyrTy 760
Db     31169 TTATAACCTTGCGATTCCTCTTGGAATCAAGTTAGAGAAACGGTTTGCAGAGCAATATTA 31228

Qy       760 rHisValValAlaMetTyrSerProAspValCysArgSerAsnProLysCysThrThrTh 780
Db     31229 TCATGTTGTAGCGATGTATTCTCCAGATGTTTGTCGTAGTAACCCCAAATGTACGACTAC 31288

Qy       780 rLeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAlaGl 800
Db     31289 CCTACTTTCCAACCAAGGGAGTTGGAAGACCAAAGGTTCGAACTTAGCAAGACAGGCTGG 31348

Qy       800 yIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsnPh 820
Db     31349 TATTGTTCAGGCCTCAGGTTTTCGATCTTTGGGAGCTGCAGCAGAGCTTTTCGGGAACTT 31408

Qy       820 eGlyPheGluTrpArgGlySerSerArgSerTyrAsnValAspAlaGlySerLysIleLy 840
Db     31409 TGGCTTTGAATGGCGGGGATCTTCTCGTAGCTATAATGTAGATGCGGGTAGCAAAATCAA 31468

Qy       840 sPhe 841
Db     31469 ATTT 31472
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RESULT 8
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LOCUS       A81855                  1830 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 29 from Patent WO9858953.
ACCESSION   A81855
VERSION     A81855.1  GI:6731880
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1830)
  AUTHORS   Madsen,A. and Birkelund,S.
  TITLE     NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA PNEUMONIAE
  JOURNAL   Patent: WO 9858953-A 29 30-DEC-1998;
            MADSEN ANNA SOFIE (DK); BIRKELUND SVEND (DK)
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                     /db_xref="taxon:32644"
     CDS             <1. .>1830
                     /note="unnamed protein product"
                     /codon_start=1
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                    GTIVFSGEKLTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQDANSKLI
                    MDLGTSLVANTESIELTNLEINIDSLRNGKKIKLSAATAQKDIRIDRPVVLAISDESF
                    YQNGFLNEDHSYDGILELDAGKDIVISADSRSIDAVQSPYGYQGKWTINWSTDDKKAT
                    VSWAKQSFNPTAEQEAPLVPNLLWGSFIDVRSFQNPIELGTEGAPYEKRFWVAGISNV
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                    GSLRLQHDASLYSVVSILLGEGGLREILLPYVSNTLPCSFYGQLSYGHTDHRMKTESL
                    PPPPPTLSTDHTSWGGYVWAGELGTRVAVENTSGRGPFREYTPFVKVQAVYSRQDSFV
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BASE COUNT      485 a    357 c    443 g    545 t
ORIGIN

Alignment Scores:
Pred. No.:              1.44e-151       Length:         1830
Score:                  2603.00         Matches:        532
Percent Similarity:     74.46%          Conservative:   22
Best Local Similarity:  71.51%          Mismatches:     50
Query Match:            60.61%          Indels:         140
DB:                     6               Gaps:           8

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Qy         30 LeuSerAlaSerAsnSerPheAspGlyThrThrSerThrThrSerPheSerSerLys--- 48
Db         10 TTAGGGAGTCGTGACAGTTATAATGGTGATACAAGCACCACAGAATTTACTCCTAAAGCG 69

Qy         49 ThrSerSerAlaThrAspGlyThrAsnTyrValPheLysAspSerValValIleGluAsn 68
Db         70 GCAACTTCTGATGCTAGTGGCACGACCTATATTCTCGATGGGGATGTCTCGATAAGCCAA 129

Qy         69 ValProLysThrGlyGluThrGlnSerThrSerCysPheLysAsnAspAlaAlaAlaGly 88
Db        130 GCAGGGAAACAA---ACGAGCTTAACCACAAGTTGTTTTTCTAAC------ACTGCAGGA 180

Qy         89 AspLeuAsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThr 108
Db        181 AATCTTACCTTCTTAGGGAACGGATTTTCTCTTCATTTTGACAATATTATTTCGTCTACT 240

Qy        109 AlaSerGlyAlaAlaIleGlySerGluAlaAlaAsnLysThrValThrLeuSerGlyPhe 128
Db        241 GTTGCAGGTGTTGTTGTTAGCAATACAGCAGCTTCTGGGATTACGAAATTCTCAGGATTT 300

Qy        129 SerAlaLeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIle 148
Db        301 TCAACTCTTCGGATGCTTGCAGCTCCTAGGACCACA---------------------- 336

Qy        149 AsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsnPhe 168
Db        336 ------------------------------------------------------------ 336

Qy        169 SerThrGlyAspGlyGlyAlaIleAsnCysAlaGlySerLeuLysIleAlaAsnAsnLys 188
Db        336 ------------------------------------------------------------ 336

Qy        189 SerLeuSerPheIleGlyAsnSerSerSerThrArgGlyGlyAlaIleHisThrLysAsn 208
Db        336 ------------------------------------------------------------ 336

Qy        209 LeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAla 228
Db        336 ------------------------------------------------------------ 336

Qy        229 GlyLysGlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSer 248
Db        337 GGTAAA---GGAGCCATTAAAATTACCGATGGT---------------------- 366

Qy        249 GlyAspIleIlePheGlu------GlyAsnThrIleGlyAlaThrGlyThrValSerHis 266
Db        367 ------CTGGTGTTTGAGAGTATAGGGAAT---------------------- 390

Qy        267 SerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyHis 286

Db        390 ------------------------------------------------------------ 390

Qy        287 ThrIleTyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeu 306
Db        391 ------------CTTGATCCGATTACTGTAACAGGATCGACATCTGTTGCTGATGCTCTC 438

Qy        307 AsnIleAsnSerProAspThrGlyAspAsnLysGluTyrThrGlyThrIleValPheSer 326
Db        439 AATATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACGGGAACCATAGTCTTTTCT 498

Qy        327 GlyGluLysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSerLysLeuLeu 346
Db        499 GGAGAGAAGCTCACGGAGGCAGAAGCTAAAGATGAGAAGAACCGCACTTCTAAATTACTT 558

Qy        347 GlnAsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAla 366
Db        559 CAAAATGTTGCTTTTAAAAATGGGACTGTAGTTTTAAAAGGTGATGTCGTTTTAAGTGCG 618

Qy        367 AsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeuVal 386
Db        619 AACGGTTTCTCTCAGGATGCAAACTCTAAGTTGATTATGGATTTAGGGACGTCGTTGGTT 678

Qy        387 AlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArgAsn 406
Db        679 GCAAACACCGAAAGTATCGAGTTAACGAATTTGGAAATTAATATAGACTCTCTCAGGAAC 738

Qy        407 GlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAspArgPro 426
Db        739 GGGAAAAAGATAAAACTCAGTGCTGCCACAGCTCAGAAAGATATTCGTATAGATCGTCCT 798

Qy        427 ValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeuAsnGluAspHis 446
Db        799 GTTGTACTGGCAATTAGCGATGAGAGTTTTTATCAAAATGGCTTTTTGAATGAGGACCAT 858

Qy        447 SerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIleSerAlaAspSer 466
Db        859 TCCTATGATGGGATTCTTGAGTTAGATGCTGGGAAAGACATCGTGATTTCTGCAGATTCT 918

Qy        467 ArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGlyLysTrpThrIleAsnTrp 486
Db        919 CGCAGTATAGATGCTGTACAATCTCCGTATGGCTATCAGGGAAAGTGGACGATCAATTGG 978

Qy        487 SerThrAspAspLysLysAlaThrValSerTrpAlaLysGlnSerPheAsnProThrAla 506
Db        979 TCTACTGATGATAAGAAAGCTACGGTTTCTTGGGCGAAGCAGAGTTTTAATCCCACTGCT 1038

Qy        507 GluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySerPheIleAspValArgSer 526
Db       1039 GAGCAGGAGGCTCCGTTAGTTCCTAATCTTCTTTGGGGTTCTTTTATAGATGTTCGTTCC 1098

Qy        527 PheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTyrGluLysArgPheTrpVal 546
Db       1099 TTCCAGAATTTTATAGAGCTAGGTACTGAAGGTGCTCCTTACGAAAAGAGATTTTGGGTT 1158

Qy        547 AlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAsnGlnArgLysPheArgHis 566
Db       1159 GCAGGCATTTCCAATGTTTTGCATAGGAGCGGTCGTGAAAATCAAAGGAAATTCCGTCAT 1218

Qy        567 ValSerGlyGlyAlaValValGlyAlaSerThrArgMetProGlyGlyAspThrLeuSer 586
Db       1219 GTGAGTGGAGGTGCTGTAGTAGGTGCTAGCACGAGGATGCCGGGTGGTGATACCTTGTCT 1278

Qy        587 LeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPheMetAsnThrAsnPheAla 606
Db       1279 CTGGGTTTTGCTCAGCTCTTTGCGCGTGACAAAGACTACTTTATGAATACCAATTTCGCA 1338

Qy        607 LysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSerLeuTyrSerValValSer 626
Db       1339 AAGACCTACGCAGGATCTTTACGTTTGCAGCACGATGCTTCCCTATACTCTGTGGTGAGT 1398

Qy        627 IleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuProTyrValSerLysThrLeu 646
Db       1399 ATCCTTTTAGGAGAGGGAGGACTCCGCGAGATCCTGTTGCCTTATGTTTCCAATACTCTG 1458
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Qy        647 ProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAspHisArgMetLysThrGlu 666
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Db       1459 CCGTGCTCTTTCTATGGGCAGCTTAGCTACGGCCATACGGATCATCGCATGAAGACCGAG 1518

Qy        667 SerLeuProProProProProThrLeuSerThrAspHisThrSerTrpGlyGlyTyrVal 686
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Db       1519 TCTCTACCCCCCCCCCCCCCCGACGCTCTCGACGGATCATACTTCTTGGGGAGGATATGTC 1578

Qy        687 TrpAlaGlyGluLeuGlyThrArgValAlaValGluAsnThrSerGlyArgGlyPhePhe 706
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Db       1579 TGGGCTGGAGAGCTGGGAACTCGAGTTGCTGTTGAAAATACCAGCGGCAGAGGATTTTTC 1638

Qy        707 GlnGluTyrThrProPheValLysValGlnAlaValTyrAlaArgGlnAspSerPheVal 726
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Db       1639 CGAGAGTACACTCCATTTGTAAAAGTCCAAGCTGTTTACTCGCGCCAAGATAGCTTTGTT 1698

Qy        727 GluLeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyrAsnLeuAlaIlePro 746
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1699 GAACTAGGAGCTATCAGTCGTGATTTTAGTGATTCGCATCTTTATAACCTTGCGATTCCT 1758

Qy        747 LeuGlyIleLysLeuGluLysArgPheAlaGluGlnTyrTyrHisValValAlaMetTyr 766
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Db       1759 CTTGGAATCAAGTTAGAGAAACGGTTTGCAGAGCAATATTATCATGTTGTTGCGATGTAT 1818

Qy        767 SerProAspVal 770
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Db       1819 TCTCCAGATGTT 1830

RESULT 9
A81835
LOCUS       A81835                 2787 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 9 from Patent WO9858953.
ACCESSION   A81835
VERSION     A81835.1  GI:6731868
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2787)
  AUTHORS   Madsen,A. and Birkelund,S.
  TITLE     NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA PNEUMONIAE
  JOURNAL   Patent: WO 9858953-A 9 30-DEC-1998;
            MADSEN ANNA SOFIE (DK); BIRKELUND SVEND (DK)
FEATURES             Location/Qualifiers
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BASE COUNT      811 a    583 c    598 g    795 t
ORIGIN

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Score:                  1569.50         Matches:        373
Percent Similarity:     52.33%          Conservative:   121
Best Local Similarity:  39.51%          Mismatches:     308
Query Match:            36.54%          Indels:         142
DB:                     6               Gaps:           19

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Qy         15 ThrLeuSerMetSerAsnLeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsn 34
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Db         34 ACATTTGCTATTTTCCCTTTGTCTATGATTGCTACCGAGACAGTTTTGGATTCAAGTGCG 93

Qy         35 SerPheAspGlyThrThrSerThrThrSerPheSerSerLysThrSerSerAlaThrAsp 54
              ||||||||||||                ::::||||||   :::   |||
Db         94 AGTTTCGATGGG---AATAAAAATGGTAATTTTTCAGTTCGTGAGAGTCAGGAAGATGCT 150

Qy         55 GlyThrAsnTyrValPheLysAspSerValValIleGluAsnValProLysThrGlyGlu 74
              ||||||   |||:::||||||   :::|||   :::||||||:::|||   ||||||
Db        151 GGAACTACCTACCTATTTAAGGGAAATGTCACTCTAGAAAATATTCCTGGAACAGGCACA 210

Qy         75 ThrGlnSerThrSerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGly 94
                 :::   |||||||||   |||              |||||||||   |||   |||
Db        211 GCAATCACAAAAAGCTGTTTTAACAAC------ACTAAGGGCGATTTGACTTTCACAGGT 264

Qy         95 GlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIle 114
              |||   |||          |||     :::||||||   |||   :::|||||||:::
Db        265 AACGGGAACTCTCTATTGTTCCAAACGGTGGATGCAGGGACTGTAGCAGGGGCTGCTGTT 324

Qy        115 GlySerGluAlaAlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeu 134
              |||          :::|||:::   |||       |||||||||:::|||||||:::
Db        325 AACAGCAGCGTGGTAGATAAATCTACCACGTTTATAGGGTTTTCTTCGCTATCTTTTATT 384

Qy        135 LysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValLys---GlyAsn 153
              ||||||   |||:::::::|||   |||   ||||||::::::          |||:::
Db        385 GCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGCCGTTAGCTGCTCTACGGGTAGC 444

Qy        154 LeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsnPheSerThrGlyAspGly 173
              |||          |||     :::|||          ||||||||||||   :::|||
Db        445 TTGAAGTTTGACAAAAATGTCAGTTTGCTCTTCAGCAAAAACTTTTCAACGGATAATGGC 504

Qy        174 GlyAlaIleAsnCys---------------------------------------------- 178
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Db        505 GGTGCTATCACCGCAAAAACTCTTTCATTAACAGGGACTACAATGTCAGCTCTGTTTTCT 564

Qy        178 ---------------------------------------------------------- 178

Db        565 GAAAATACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTACCATTACT 624

Qy        178 ---------------------------------------------------------- 178

Db        625 GGAAACCAAGGGGAAGTCTCTTTTTCTGACAATACTTCTTCGGATTCTGGAGCTGCAATT 684

Qy        179 ------AlaGlySerLeuLysIleAlaAsnAsnLysSerLeuSerPheIle--------- 193
                    |||:::  |||:::||||||      :::||||||||
Db        685 TTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTTCCTTTATTGACAATAAG 744

Qy        193 ---------------------------------------------------------- 193

Db        745 GTCACAGGAGCGAGCTCCTCAACAACGGGGGATATGTCAGGAGGTGCTATCTGTGCTTAT 804

Qy        194 ----------------------------------------------------------Gly 194

Db        805 AAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAGCAAC 864

Qy        195 AsnSerSerSerThrArgGlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGly 214
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Db        865 AATACATCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTCCGGA 924

Qy        215 GlyGluThrLeuPhe---------------GlnGlyAsnThrAlaProThrAlaAlaGly 229
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Db        925 GGACTTACCCTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCT------------ 972

Qy        230 LysGlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGly 249
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Db        973 AAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGGT 1032

Qy        250 AspIleIlePheGluGlyAsnThrIleGlyAlaThr------GlyThrValSerHisSer 267
              ||||||:::|||   ||||||||:::   :::|||       ||||||   :::   |||
Db       1033 GACATTGTCTTTTTAGGGAATACAGTCACTTCTACTACTCCTGGGACG---AATAGAAGT 1089

Qy        268 AlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyHisThr 287
              :::||||||||||||||||||||:::|||||||||||:::|||   |||
Db       1090 AGTATCGACTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTGCTGGTAGAGCC 1149

Qy        288 IleTyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsn 307
              ||||||||||||||||||||||        ||||||:::|||   |||   |||
Db       1150 ATCTACTTCTATGATCCCATAACTACAGGATCTTCCACAACAGTTACAGATGTCTTAAAA 1209

Qy        308 IleAsnSerProAspThrGlyAspAsnLysGluTyrThrGlyThrIleValPheSerGly 327
              :::|||                  :::||||||||   |||:::|||:::|||
Db       1210 GTTAATGAGACTCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAGGA 1269
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Qy       328 GluLysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSerLysLeuLeuGln 347
Db      1270 GAAAAGTTATCAGAGACAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAG 1329

Qy       348 AsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsn 367
Db      1330 CCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAACATGGAGTGACTCTGCAGACTCAG 1389

Qy       368 GlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeu---Val 386
Db      1390 GCATTCACTCAACAGGCAGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAACCT 1449

Qy       387 AlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArgAsn 406
Db      1450 GCTGATACTAGCACCATA------AACAATTTGGTCATTAACATCAGTTCTATAGACGGT 1503

Qy       407 GlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAspArgPro 426
Db      1504 GCAAAGAAGGCAAAAATAGAAACCAAAGCTACGTCAAAAAATCTGACTTTATCTGGAACC 1563

Qy       427 ValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeuAsnGluAspHis 446
Db      1564 ATCACTTTATTGGACCCGACGGGCACGTTTTATGAAAATCATAGTTTAAGAAATCCTCAG 1623

Qy       447 SerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIleSerAla--AspS 466
Db      1624 TCCTACGAC---ATCTTAGAGCTCAAAGCTTCTGGAACTGTAACAAGCACCGCAGTGACT 1680

Qy       466 erArgSerIleAspAlaValGlnSerPro-TyrGlyTyrGlnGlyLysTrp---ThrIle 484
Db      1681 CCAGATCCTATAATGGGTGAGAAATTCCATTACGGCTATCAGGGAACTTGGGGCCCAATT 1740

Qy       485 AsnTrpSerThrAsp---AspLysLysAlaThrValSerTrpAlaLysGlnSerPheAsn 503
Db      1741 GTTTGGGGGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAAAACTGGCTATATT 1800

Qy       504 ProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySerPheIleAsp 523
Db      1801 CCTAATCCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCATTTATAGAT 1860

Qy       524 ValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTyrGluLysArg 543
Db      1861 ATTAGCTCTCTCCATTATCTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGACCGTGCT 1920

Qy       544 PheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAsnGlnArgLys 563
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  AUTHORS   Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Hyman,R.W.,
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  TITLE     Comparative genomes of Chlamydia pneumoniae and C. trachomatis
  JOURNAL   Nat. Genet. 21 (4), 385-389 (1999)
  MEDLINE   99206606
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            Grimwood,J., Davis,R.W. and Stephens,R.S.
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  JOURNAL   Submitted (01-DEC-1998) Program in Infectious Diseases, University
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BASE COUNT 4710 a 3330 c 3665 g 4743 t
ORIGIN

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US-09-830-446-27 (1-841) x AE001587 (1-16448)

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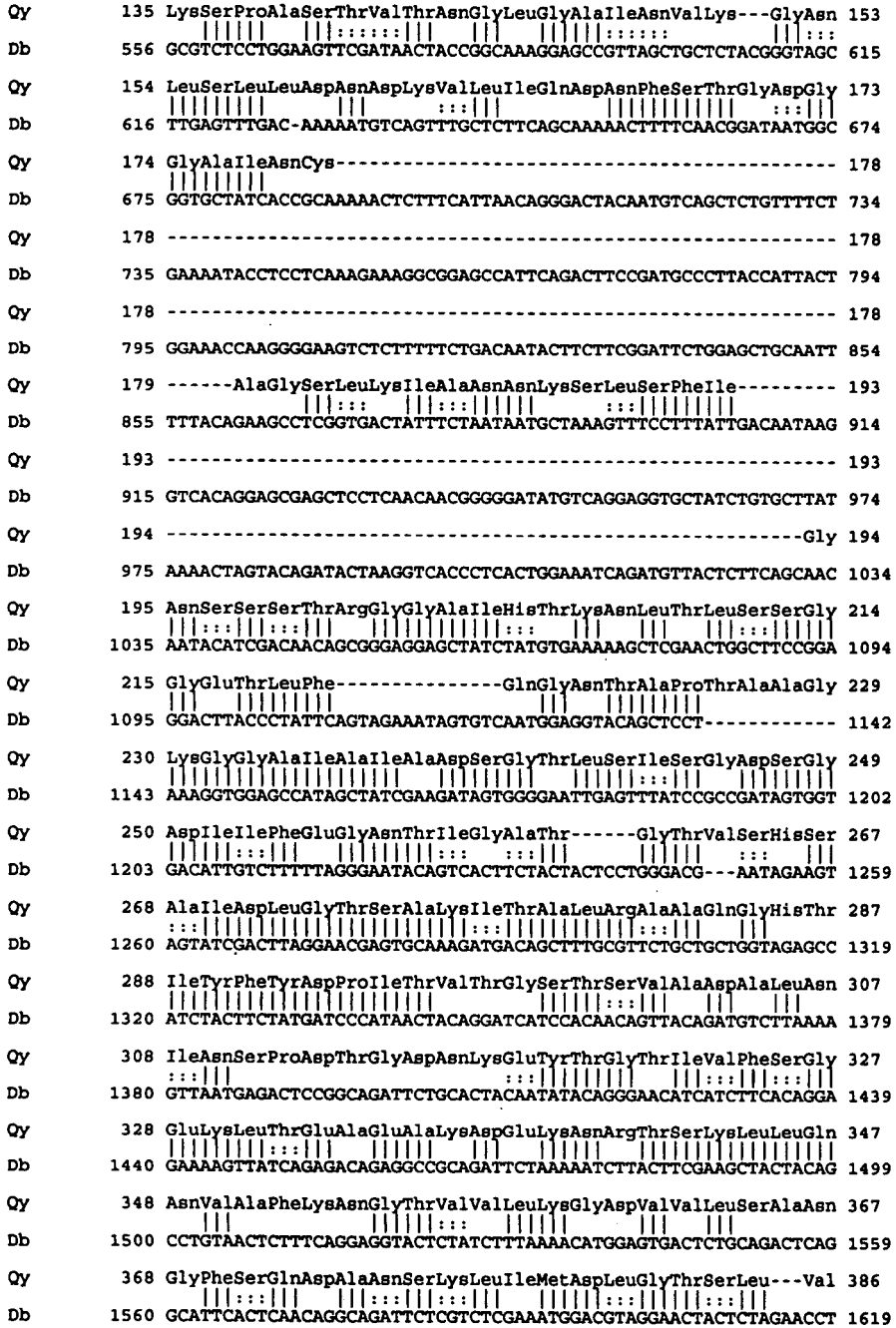
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DEFINITION  Sequence 22 from Patent WO02053588.
ACCESSION   AX662085
VERSION     AX662085.1  GI:29163040
KEYWORDS    .
SOURCE      Chlamydophila psittaci
  ORGANISM  Chlamydophila psittaci
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
REFERENCE   1
  AUTHORS   Johnston,S.A., Stemke-Hale,K., Sykes,K.F. and Kaltenboeck,B.
  TITLE     Methods and compositions for vaccination comprising nucleic acid
            and/or polypeptide sequences of chlamydia psittaci
  JOURNAL   Patent: WO 02053588-A 22 11-JUL-2002;
            BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
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US-09-830-446-27 (1-841) x AX662085 (1-2520)

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DEFINITION Sequence 22 from Patent WO0247718.
ACCESSION AX666157
VERSION AX666157.1 GI:29290977
KEYWORDS .
SOURCE Chlamydophila psittaci
ORGANISM Chlamydophila psittaci
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
REFERENCE 1
AUTHORS Johnston,S.A.
TITLE Methods and compositions for vaccination comprising nucleic acid ad/or polypeptide sequences of _i(chlamydia)
JOURNAL Patent: WO 0247718-A 22 20-JUN-2002;
BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
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US-09-830-446-27 (1-841) x AX666157 (1-2520)

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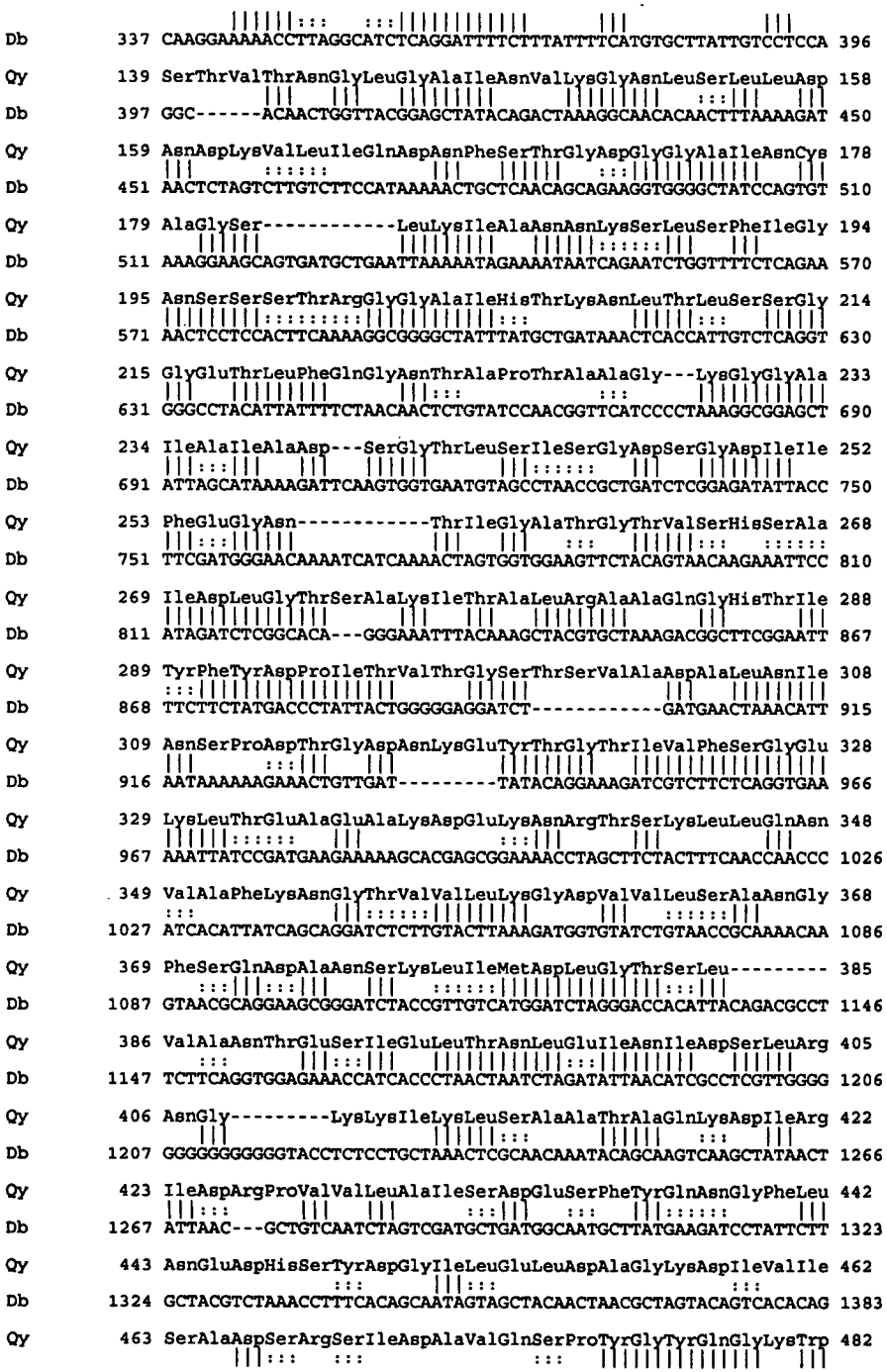
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  TITLE     Identification of a multigene family coding for the 90 kDa proteins
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REFERENCE   2  (sites)
  AUTHORS   Longbottom,D., Russell,M., Dunbar,S.M., Jones,G.E. and Herring,A.J.
  TITLE     Molecular cloning and characterization of the genes coding for the
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  JOURNAL   Infect. Immun. 66 (4), 1317-1324 (1998)
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  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-1996) Moredun Research Institute, International
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Alignment Scores:
Pred. No.:                1.03e-82        Length:         6110
Score:                    1497.00         Matches:        357
Percent Similarity:       56.21%          Conservative:   132
Best Local Similarity:    41.03%          Mismatches:     321
Query Match:              34.85%          Indels:         60
DB:                       1               Gaps:           25

US-09-830-446-27 (1-841) x CPU65942 (1-6110)

Qy          1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
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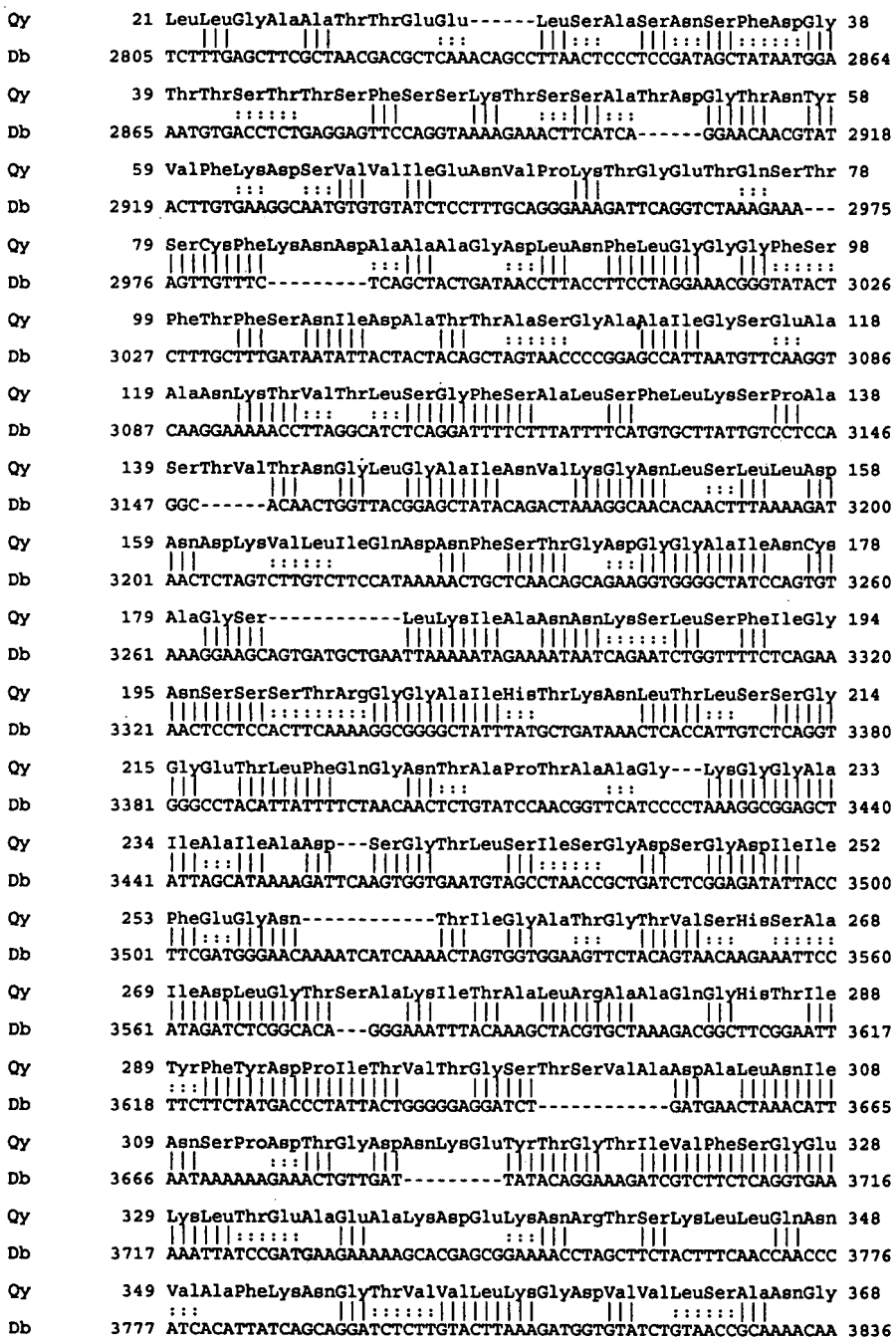
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Qy 59 ValPheLysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThr 78
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Qy 79 SerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSer 98
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Db 3147 GGC------ACAACTGGTTACGGAGCTATACAGACTAAAGGCAACACAACTTTAAAAGAT 3200
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Db 3201 AACTCTAGTCTTGTCTTCCATAAAAACTGCTCAACAGCAGAAGGTGGGGCTATCCAGTGT 3260
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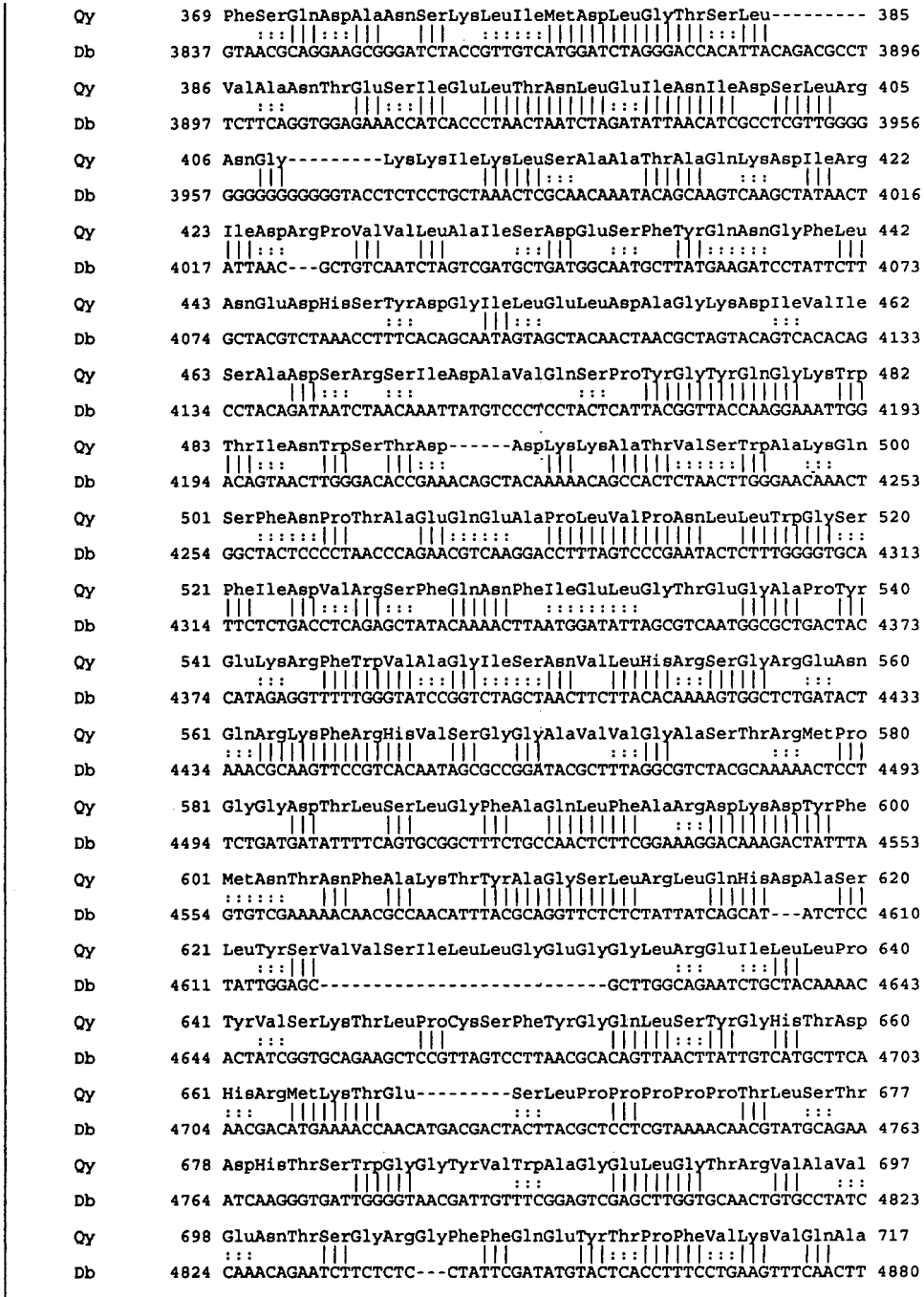
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            precursor, genes, complete cds.
ACCESSION   U65943
VERSION     U65943.1  GI:1617508
KEYWORDS    .
SOURCE      Chlamydophila abortus
  ORGANISM  Chlamydophila abortus
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
REFERENCE   1  (sites)
  AUTHORS   Longbottom,D., Russell,M., Jones,G.E., Lainson,F.A. and
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  TITLE     Identification of a multigene family coding for the 90 kDa proteins
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  JOURNAL   FEMS Microbiol. Lett. 142 (2-3), 277-281 (1996)
  MEDLINE   96406378
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REFERENCE   2  (sites)
  AUTHORS   Longbottom,D., Russell,M., Dunbar,S.M., Jones,G.E. and Herring,A.J.
  TITLE     Molecular cloning and characterization of the genes coding for the
            highly immunogenic cluster of 90-kilodalton envelope proteins from
            the Chlamydia psittaci subtype that causes abortion in sheep
  JOURNAL   Infect. Immun. 66 (4), 1317-1324 (1998)
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REFERENCE   3  (bases 1 to 6234)
  AUTHORS   Longbottom,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-1996) Moredun Research Institute, International
            Research Centre, Pentlands Science Park, Bush Loan, Penicuik,
            Midlothian EH26 0PZ, UK
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Alignment Scores:
Pred. No.:                1.06e-82      Length:          6234
Score:                    1497.00       Matches:         357
Percent Similarity:       56.21%        Conservative:    132
Best Local Similarity:    41.03%        Mismatches:      321
Query Match:              34.85%        Indels:          60
DB:                       1             Gaps:            25

US-09-830-446-27 (1-841) x CPU65943 (1-6234)

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Qy         21 LeuLeuGlyAlaAlaThrThrGluGlu------LeuSerAlaSerAsnSerPheAspGly 38
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Qy         39 ThrThrSerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyr 58
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Qy         99 PheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAla 118
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Qy        119 AlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAla 138
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Qy        215 GlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGly---LysGlyGlyAla 233
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Qy        269 IleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyHisThrIle 288
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Qy        289 TyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsnIle 308
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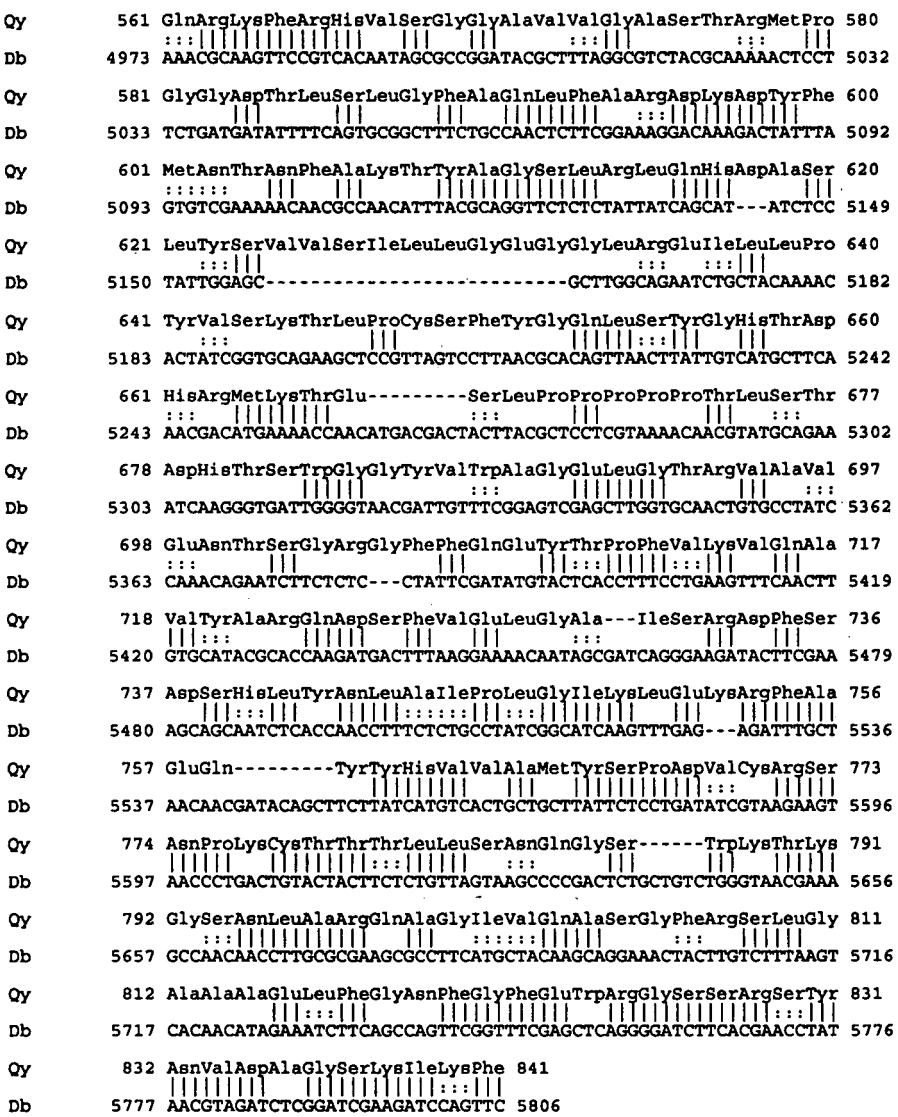

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VERSION     AX349593.1  GI:18615403
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SOURCE      Chlamydophila pneumoniae
  ORGANISM  Chlamydophila pneumoniae
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
REFERENCE   1
  AUTHORS   Ratti,G. and Grandi,G.
  TITLE     Immunisation against Chlamydia pneumoniae
  JOURNAL   Patent: WO 0202606-A 116 10-JAN-2002;
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Best Local Similarity:    35.90%          Mismatches:      335
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US-09-830-446-27 (1-841) x AX349593 (1-2787)
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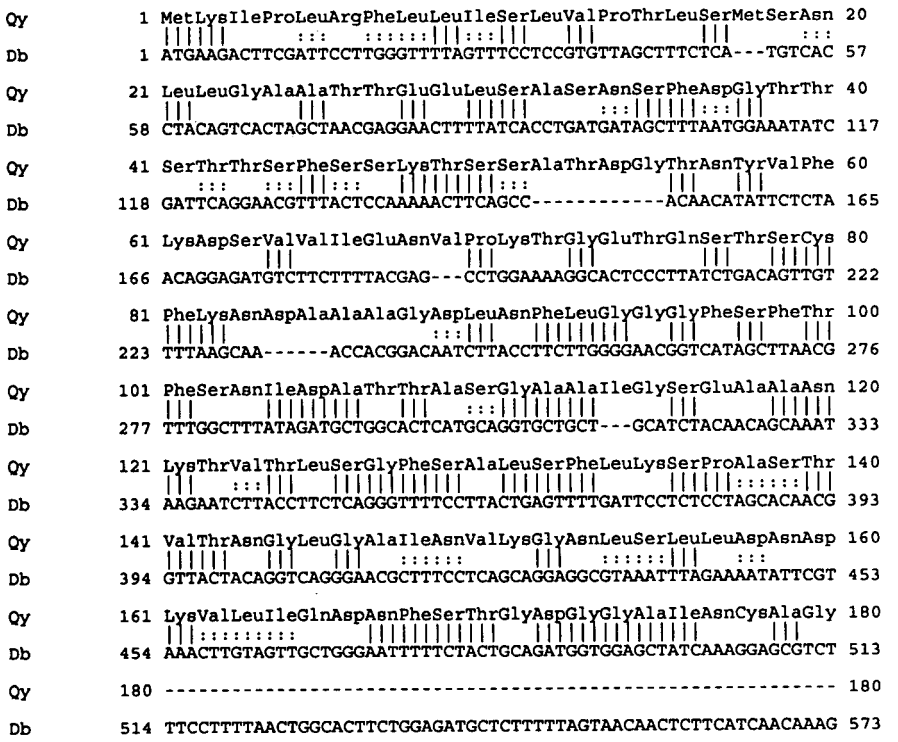

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Qy         141 ValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAsp 160

Db         394 GTTACTACAGGTCAGGGAACGCTTTCCTCAGCAGGAGGCGTAAATTTAGAAAATATTCGT 453

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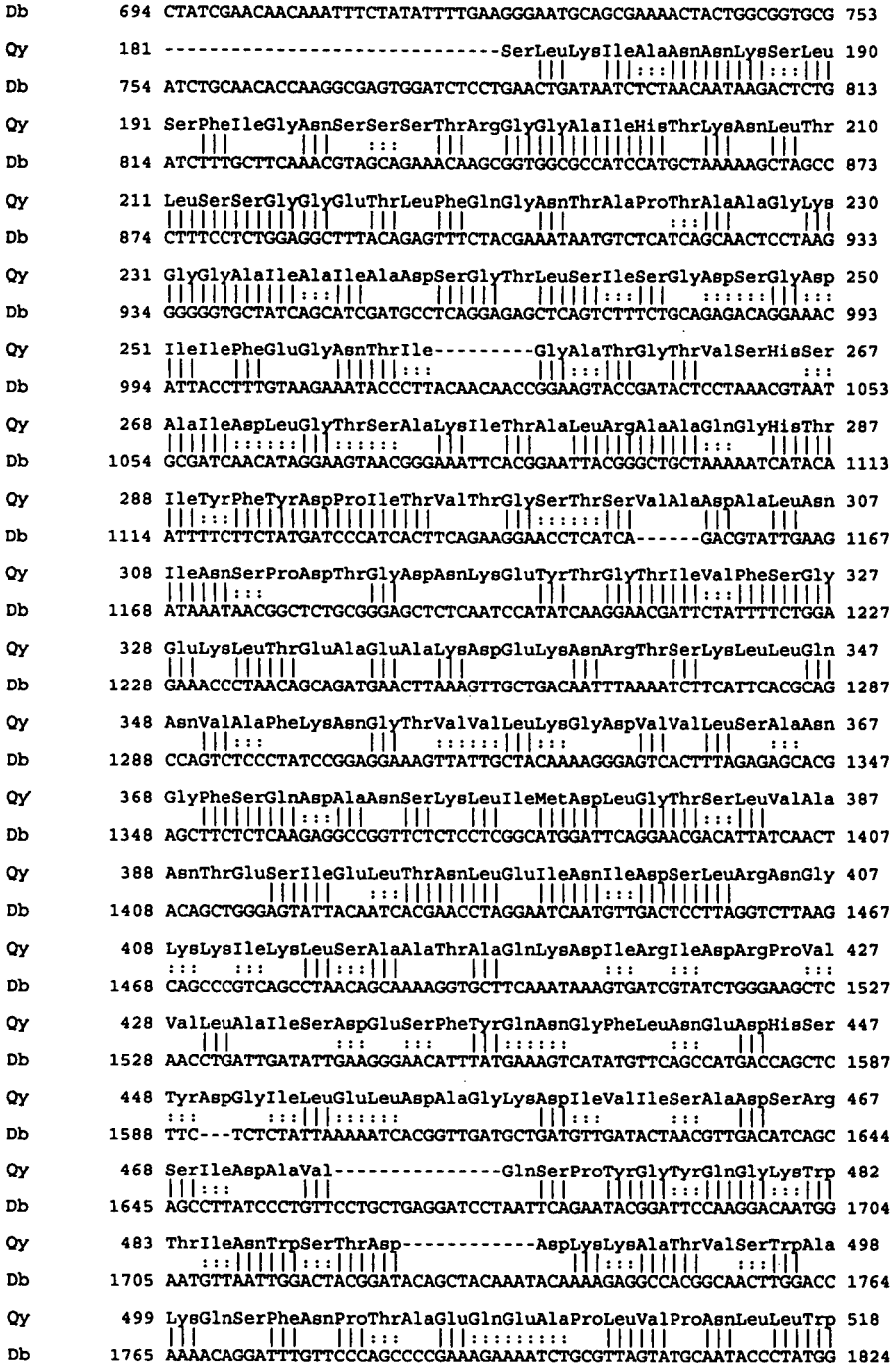

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Job time : 8190 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 29, 2004, 10:21:11 ; Search time 121 Seconds
(without alignments)
3067.795 Million cell updates/sec

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Perfect score: 4295
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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	1365	31.8	1230025	4	US-09-198-452A-1	Sequence 1, Appli
3	939	21.9	3021	4	US-09-556-877-182	Sequence 182, App
4	939	21.9	3021	4	US-09-620-412C-182	Sequence 182, App
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6	936	21.8	2949	4	US-09-556-877-170	Sequence 170, App
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43	266	6.2	1965	4	US-09-598-419-340	Sequence 340, App
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45	266	6.2	2052	4	US-09-598-419-356	Sequence 356, App

ALIGNMENTS

RESULT 1
US-09-198-452A-1
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pre
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
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Qy        201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220
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Db      29549 GGCGGAGCGATTCATACCAAAAACCTCACACTATCTTCTGGTGGGGAAACTCTATTTCAG 29608

Qy        221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240
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Db      29609 GGGAATACAGCGCCTACGGCTGCTGGTAAAGGAGGTGCTATCGCGATTGCAGACTCTGGC 29668

Qy        241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260
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Db      29669 ACCCTATCCATTTCTGGAGACAGTGGCGACATTATCTTTGAAGGCAATACGATAGGAGCT 29728

Qy        261 ThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeu 280
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Db      29729 ACAGGAACCGTCTCTCATAGTGCTATTGATTTAGGAACTAGCGCTAAGATAACTGCGTTA 29788

Qy        281 ArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGlySerThr 300
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Db      29789 CGTGCTGCGCAAGGACATACGATATACTTTTATGATCCGATTACTGTAACAGGATCGACA 29848

Qy        301 SerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGluTyrThr 320
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Db      29849 TCTGTTGCTGATGCTCTCAATATTAATAGCCCTGATACTGGAGATAACAAAGAGTATACG 29908

Qy        321 GlyThrIleValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGluLysAsn 340
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Db      29909 GGAACCATAGTCTTTTCTGGAGAGAAGCTCACGGAGGCAGAAGCTAAAGATGAGAAGAAC 29968

Qy        341 ArgThrSerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeu-LysGl 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db      29969 CGCACTTCTAAATTACTTCAAAATGTTGCTTTTAAAAATGGGACTGTAGTTTTGAAAAGG 30028

Qy        360 yAspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAs 380
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Db      30029 TGATGTCGTTTTAAGTGCGAACGGTTTCTCTCAGGATGCAAACTCTAAGTTGATTATGGA 30088

Qy        380 pLeuGlyThrSerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAs 400
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Db      30089 TTTAGGGACGTCGTTGGTTGCAAACACCGAAAGTATCGAGTTAACGAATTTGGAAATTAA 30148

Qy        400 nIleAspSerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAs 420
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Db      30149 TATAGACTCTCTCAGGAACGGGAAAAAGATAAAACTCAGTGCTGCCACAGCTCAGAAAGA 30208

Qy        420 pIleArgIleAspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGl 440
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Db      30209 TATTCGTATAGATCGTCCTGTTGTACTGGCAATTAGCGATGAGAGTTTTTATCAAAATGG 30268

Qy        440 yPheLeuAsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIl 460
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Db      30269 CTTTTTGAATGAGGACCATTCCTATGATGGGATTCTTGAGTTAGATGCTGGGAAAGACAT 30328

Qy        460 eValIleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGl 480
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Db      30329 CGTGATTTCTGCAGATTCTCGCAGTATAGATGCTGTACAATCTCCGTATGGCTATCAGGG 30388

Qy        480 yLysTrpThrIleAsnTrpSerThrAspAspLysLysAlaThrValSerTrpAlaLysGl 500
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Qy        500 nSerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySe 520
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Qy        520 rPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTy 540
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Qy        540 rGluLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAs 560
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Qy        560 nGlnArgLysPheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArgMetPr 580
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Qy        580 oGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPh 600
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Qy        600 eMetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSe 620
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Qy        620 rLeuTyrSerValValSerIleLeuLeuGlyGluGlyGlyLeuArgGluIleLeuLeuPr 640
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Qy        660 pHisArgMetLysThrGluSerLeuProProProProProThrLeuSerThrAspHisTh 680
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Qy        680 rSerTrpGlyGlyTyrValTrpAlaGlyGluLeuGlyThrArgValAlaValGluAsnTh 700
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Db      30989 TTCTTGGGGAGGATATGTCTGGGCTGGAGAGCTGGGAACTCGAGTTGCTGTTGAAAATAC 31048

Qy        700 rSerGlyArgGlyPhePheGlnGluTyrThrProPheValLysValGlnAlaValTyrAl 720
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Db      31049 CAGCGGCAGAGGATTTTTCCAAGAGTACACTCCATTTGTAAAAGTCCAAGCTGTTTACGC 31108

Qy        720 aArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSerAspSerHisLe 740
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Qy        740 uTyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPheAlaGluGlnTyrTy 760
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Qy        760 rHisValValAlaMetTyrSerProAspValCysArgSerAsnProLysCysThrThrTh 780
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Db      31229 TCATGTTGTAGCGATGTATTCTCCAGATGTTTGTCGTAGTAACCCCAAATGTACGACTAC 31288

Qy        780 rLeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAlaGl 800
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Qy        820 eGlyPheGluTrpArgGlySerSerArgSerTyrAsnValAspAlaGlySerLysIleLy 840
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Qy        840 sPhe 841
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Db      31469 ATTT 31472
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RESULT 2
US-09-198-452A-1/c
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae
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